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(MERI ) MERCK & CO INC
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-Q=/cgn2_1/USFTO_spool_D/US10054683/runat_10012005_174509_15490/app_query.fasta_1.2823
-Q=/cgn2_1/USFTO_spool_D/US10054683/runat_10012005_174509_15490/app_query.fasta_1.2823
-DEAA_Geneseq_23Sep04_OFWT=fastan -SUFFTX=n2p.rag -MINNATCH=0.1 -LOOPCL=0
-LIST=E45_DOCALIGN=200 -THR_SCORE=pct -THR_MATS=100 -THR_MIN=0
-MODEL=LOCAL_OUTFMT=pct -NORM=ext -HEAFSTZE=500 -MINLEN=0
-NADEL-COLAL_OUTFMT=pct -NORM=ext -HEAFSTZE=500 -MINLEN=0
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-NORM=D-COLAL_OUTFMT=DSPENCE=100 -NGGAPET=0
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAROP=10 -XGAPEXT=0.5 -FGAPOP=6
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        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                           protein search, using frame plus n2p model
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                                          Human PH30 beta chain sperm protein, having a FEE integrin binding domain, is 58.9% identical to mouse and 56.5% identical to guinea pig PH30 beta. The protein may be produced recombinantly and used in a contraceptive composition containing an effective adjuwant and an amount of sperm protein which is effective for the stimulation of antibodies which bind to sperm protein—in willow, thereby preventing or substantially reducing the rate of sperm-egg fusion
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Human and mouse sparm_protein PH30 beta chain and related contraceptive vaccines.
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                         Example 2; Page 45-48; 85pp; English
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                                                640
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                             AATGATAGAGGTGTATGCAATAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTACCT
ProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsnPhe
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                                                                                                                                                                                                                                       Human cancer/testis antigen - SEQ ID No 19.
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FOUND INC.
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20-APR-2001; 2001US-0285154P.
05-OCT-2001; 2001US-0327432P.
22-JAN-2002; 2002US-00054683.
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          661 ProProValAlalleProAlaArgLeuProGluArgArgTyr1leGluAsn1leTyrHis
                                           SerLysProMetArgTrpProPhePheLeuPheIleProPhePheIleIlePheCysVal
                                  Gorbatcheva
Anderson D;
                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid molecule, useful for diagnosing or treating
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onsey AM, Glatt K, Zhao X,
                                                                                                                SerSerAspGluGlnProGluSerGluSerGluProLysGly
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                                                                                                                                                         ADB75186 standard; protein; 734
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25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
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, Kamatkar S, W
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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal control non-prostate cancer useful for diagnosing or treating prostate cancer.

Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in the prostate cancer, and may be useful in gene therapy. Sequences given in cancer their patient form part of the printed specification, but was obtained in electronic format directly from WIPO at

Sequence 734 Alignment Scores:

1032 ACTTATGATGACATTAACAAATGCCAGTGCTCAGGAGCTGTCTGCATTATGAATCCAGAA 1091	ALALIERISPRESETVIVALLYSELIEPRESETABRICYBSETFRESIUABBFREALAHIS 3 TITATITCAAAGCAGAGTCCCAGTGTCTTCACAATCAGCCTCGCTTAGATCCTTTTTTC 1	AAACAGCAGCAGTGTGGGTAATGCAAAGCTGGAAGAGGAGGAGGAGGAGTGTGGGG 12 	ACTGAACAGATTGTGCCCTTATTGGAAAACATGCTGTGATATTGCCACATGTAATTT 13 [	32 AAAGCCGGTTCAAACTGTGCTGAAGAACCATGCTGCGAAACTGCTGTTTTATGTCAAA 13 	GAAAGATGTGTGGCCTTCCTTTGAAGATGCGACCTCCCTGAATATGCATGGATGATTG 	TCTGCATCATGCCCAGAAACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAATCAA	TGGATCTGTATAGATGAGTTTGTATGAGTGGGATAAACAATGTACAGACACATTTGGC 1 	AAAGAAGTAGAGTTTGGCCCTTCAGAATGTTATTCTCACCTTAATTCAAGACTGATGTA 	5 4	92 TGCGGAAATTAATATGTAAATATGTAGGTAAATTTTTATTACAAATTCCAAGAGCCACT 1 			1872 AGGAATCAAAGATGTGTGAGTTCTTCATACTTGGGTTATGTACTGCTGACTGA	1932 AATGATAGAGGTGTATGCAATAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTACCT 1991 	1992 CCAGATIGCTCAGTICAATCAGTCTAIGGCCTGGTGGGAGTATTGACAGTGGCAATTTT 2051 	2052 CCACCTGTAGCTATACCAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCAT 2111	2112 TCCAAACCAATGAGATGGCCATTTTTCTTATTCATTCCTTTCTTT
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Pred. No.: 0 Length: 734 Score: 3984.00 Matches: 734 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismaches: 0 Query Match: 83.07\$ Indels: 0 DB: 7	US-10-054-683-18 (1-2640) x ADB75186 (1-734)  Qy 72 ATGTGGGTTGTTTTTGCTCAGCGGGCTGGGGATGGACAGTAATTTTGAT 131	16GAAGO          sGluG]	CATATACTGTGAATT               roTyrThrValAsnLe	Qy       252 CAAAAAAACTITITACCCCATAATITIAGAGTITACAGTIATAGTGGCACAGGAATTATG       311         Db       61 GlnLysAsnPheLeuProHisAsnPheArgValTyrSerTyrSerGlyThrGlyIleMet       80	Qy 312 AAACCACTIGACCAAGATTITCAGAATTICTGCCACTACCAAGGGTATATIGAAGGTTAT 371	CCAAAATCTGTGGTGATGGTTAGCACATGTACTGGACTCAGGGGGGGG	######################################	492 CAAGTAAAACATAAGAAGCAGATGTTTCCTTATATAATGAGAAGGATATTGAATCAAGA		612 ATGCATGTATAGTTGAAAACAATTGTATAATCATATGGGGTCTGATACAACTGTTGTC 67	72 GCTCAAAAAGTTTTCCAGTTGAATTGACGAATGCTATTTTTGTTTCATTTAA 	732 ACAATTATTCTGTTTCGTTGGAGCTTTGGATGAAAATAAAATTGCAACCACTGGA 79 	Qy         792 GAAGCTAATGAGTTATTACACACATTTTTAACATGGAAAACATCTTATCTTGTTTTACGT         BS1           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	BS2 CCTCATGATGTGGCATTTTACTTGTTACAGAGAAAGTCAAATTATGTTGGTGCAACC 91	912 TITCAAGGAAGATGTGTGATGCAACTATGCAGAGGTGTTCTGCACCCCCAGAACC 9	201 FIREGINGLYBYSMELLYBANSDALAABBILYJALGGLYGLYGLYGLYGLDEUDLBFFLOALGJINL 30	Db 301 IleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIle 320

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                                        CTGATTGCTATAATGGTGAAAGTTAATTTCCAAAGGAAAAAATGGAGAAACTGAGGACTAT
nucleic acid molecule, useful for diagnosing or treating prostate
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Anderson D;
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22-MG-2001; 2001US-0314366P.
25-SEP-2001; 2001US-03141146P.
12-DEC-2001; 2001US-0362158P.
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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal control non-prostate cancer.

Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequence given in ADB75531 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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  701 ValLeulleAlaIleMetValLysValAsnPheGlnArgLysLysTrpArgThrGluAsp 720
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                                                                                        ADB75182 standard; protein; 753
                                                                                                                                                          Prostate cancer marker protein.
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-032020P.
12-DEC-2001; 2001US-0341746P.
05-WAR-2002; 2002US-0362158P.
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Mouse PH30 beta chain sperm protein, having a QDE integrin binding domain, is 55.2% identical to guinea pig PH30 beta. The protein may be produced recombinantly and used in a contraceptive composition containing an effective adjuvant and an amount of sperm protein which is effective for the stimulation of antibodies which bind to sperm protein in vivo, thereby preventing or substantially reducing the rate of sperm-egg fusion
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GCCAGTGATCATGCAGACAGCCAAAAGATGTGGATAAAAGATGGAACTTCTTGTGGTTCA
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polypeptides are used to identify modulators. A peptide, phosphopeptide, small organic molecule or an antibody is used to inhibit aberrant activity of a 55294 or 56629-expressing cell, located in a cancerous or pre-cancerous tissue. A compound that modulates the activity or expression of the polynuclectides are used to treat or prevent a disorder characterized by aberrant activity of a 56294 or 56629-expressing cell, in a subject. The present sequence represents the human 56294 protein 820 318 132 266 62 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-820)US-10-054-683-18 (1-2640) x ABR39696 1.01e-127 1530.00 57.84% 40.87% 31.90% ArgThrArgGlyCys-Percent Similarity: Best Local Similarity: Query Match: DB: 820 AA; gnment Scores: 32 Sequence 20 ø 99 22 89 231 72 92 291 112 131 351 411 151 471 171 531 191 211 231 582 969 969 251 No.: 8888888888888 유 ò 욥 셤 ò ઠે ò g 8 各 ò 셤 ઠે g 6 8 6 QQ ઠે g õ 8 8 8 à Q ò

936 816 291 876 311 351 271 331 1056 487 966 371 391 1176 411 1233 429 448 1353 1410 1470 507 1530 1590 1650 1707 467 547 1961 1827 587 607 \_ ∂ ે 셤 ò 셤 ò g ò g 8 8 8 원장 g 4 6 6 6 6 6 8 3 8 5 8 5 8 5 8 දු දු AGTAATITIGATAGTTTACCTGTGCAAATTACAGTTCCGGAGAAAATACGGTCAATAATA 179 290 350 130 470 |||| | ProAlaValProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThr 230 GGATTGACGAATGCTATTTTGTTTCATTTAATATTACAATTATTCTGTCTTCATTGGAG 755 815 ------rrpGlnProArgSer 31 51 91 CGCACTTCCAACTGCCCTGTAACCACCAACTGCCCTTATTCCGGCTGGGACCCAAGGACTT AAGGAAGGAATTGAA----TCGCAGGCATCCTACAAAATTGTAATTGAAGGGAAA AsnAspSerSerGlulleGluTyrGluGlnIleSerTyrIleIleProlleAspGluLys **CCATATACTGTGAATTTAATGCAAAAAACTTTTTACCCCATAATTTTAGAGTTTACAGT** |||::: |TyrAsn---GlnGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyr TATAGTGGCACAGGAATTATGAAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTAC CAAGGGTATATTGAAGGTTATCCAAAATCTGTGGTGATGGTTAGCACATGTACTGGACTC AGGGGCGTACTACAGTTTGAAAATGTTAGTTATGGAATAGAACCCCTGGAGTCTTCAGTT GGCTTTGAACATGTAATTTACCAAGTAAAACATAAGAAAGCAGATGTTTCCTTATAAT GAGAAGGATATTGAATCAAGA------GATCTGTCCTTTAAATTACAAAGCGCAGAG CCACAGCAAGAT-----TITGCAAAGTATATAGAAATGCATGTTATAGTTGAAAAACAA CTTTGGATAGATGAAAATAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACACACA TTGTATAATCATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTCCAGTTGATT CAAGCCATGTGGGTCTTGTTT---CTGCTCAGCGGGCTCGGCGGGCTGCGATGGAC-

1055 1115 1175 1232 1292 1352 1409 1469 1649 1706 935 350 370 GTTTGTATGAGTGGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTTGGC 1589 1886 410 428 466 486 526 999 ||||||| PheLeuGluTrpLysGlnSerTyrLeuAsnLeuArgProHisAsp11eAlaTyrLeuLeu :::||| ::: ||IeTyrMetAspTyrProArgTyrLeuGlyAlavalPheProGlyThrMetCysIleThr 1116 ATCTTTAGTAACTGCAGCTTCGAAGACTTTTGCACATTTTTGAAAGCAGAAGTCCCAG TITITAAGAIGGAAAACAICTIATCTIGITTIACGICCICAIGAIGIGGCAITTIACTI GTTTACAGAGAAAAGTCAAATTATGTTGGTGCAACCTTTTCAAGGGAAAGATGTGTGATGCA ATTITAGCTCAATTATTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAAATGC CAGTGCTCAGGAGCTGTCTGCATTATGAATCCAGAAGCAATTCATTTCAGTGGTGTGAAG AATGCAAAGCTGGAAGCAGGAGGAGTGTGACTGTGGGACTGAACAGGATTGTGCCCTT ATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCCT AACTAIGCAGGAGGIGTIGTICTGCACCCCAGAACCATAAGTCTGGAATCACTTGCAGTT TGTCTTCACAATCAGCCTCGCTTAGATCCTTTTTTCAAACAG---CAAGCAGTGTGTGGT ::||||||||||| ---ProAlaSerCysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyr TCCTTTGAAGAATGCGACCTCCCTGAATATTGCAATGGATCATCTGCATCATGCCCAGAA :::
AlaHisProGluCysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyPro CCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTGGAAACTGTGGTATA AGT---GATTCAGGATACACACAGTGTGAAGCTGACAATCTGCAGTGCGGAAAATTAATA :::
ValArgAspSerValCysIleThrValAspTyrLysbeuProArgThrValProAspPro AACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGA 527 AspCysHisAspLeuAspAlaArgCysGluSerValPheGlybysGlySerArgAsnAla TGTAAATATGTAGGTAAATTTTTATTACAAATTCCAAGAGCCACTATTATTGCCAAC CysThrTyrProThrArgLysProPheHisGlnGluAsnGlyAspValileTyrAlaPhe ATGTGGATAAAAGATGGAACTTCTTGTGGTTCAAATAAGGTTTGCAGGAATCAAAGATGT ATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGTGATCATGCAGACAGCCAAAAG ::

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360 ATTGAAGGTTATCCAAAATCTGTGGTGATGGTTAGCACATGTACTGGACTCAGGGGCGTA 419
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Best Local Similarity:
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N-PSDB; ABK33580
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                                                 GTGAGTTCTTCATACTTG------GGTTATGATTGTACTACTGAAATGCAATGAT 1937
                                                                                   CysGlnIleArgSer-----LysGlyPheSerilePheProGluGluAspMetGly 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              709 SerGlyLysThrGluAsnThrTrpLeuLeuGlyPheLeulleAlaLeuProlleLeulle 728
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breatc cancer; prostate tumour; rectal tumour; liver tumour;
pericyte call proliferation; chondrocyte call proliferation;
tumour necrosis factor-alpha.
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2000US-0220664P
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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosting tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast calls. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO protein sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
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Wood WI;
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ValHisLeulysGlnArgTyrPheLeuAlaAspAsnPheMetIleTyrLeuTyrAsn---
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01-MAR-2001; 2001WO-US006666.
22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001WO-US017092.
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| CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaH1sProGlu
LeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaValGluPheGln
                                                                                                                                                                                   181 ProAspLeuPheProLeuTyrLeuGluMetHis1leValValAspLysThrLeuTyrAsp
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161 LeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal
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                                                                                                                                                                                                                                                                                    One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                  Gerritsen ME, Goddard A, Godowski Po
Smith V, Stephan JF, Watanabe CK,
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Grimaldi JC, Gurney
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N-PSDB; ACA66885.
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cal Similarity:
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01-JUN-2001;
29-JUN-2001;
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01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH ) GENENTECH INC

12-AUG-2002; 2002US-00218631,

US2003045687-A1.

06-MAR-2003

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1658
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1542 GGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTTGGCCCTTCAGAATGT 1601
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                                                         498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys
                                                                                                                                                         538 LysTyrvalPheCysGlyTrpArgAsnLeulleCysGlyArgLeuValCysThrTyrPro
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arthritis; wound

Homo sapiens

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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, blosensors or bioreactors. These are cumulative useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, rectal tumour, or liver tumour) in amamal, for stimulating the release of TNF-alpha from human blood, or cornal human dermal fibrolliferation or differentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating normal fibrollate proliferation. The PRO nucleic acid or cornal human dermal fibrollate proliferation of pericyte cells, or for modulating colypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets of the presence of these diseases. The PRO polypeptides are destinantiation of the presence of these diseases. The PRO polypeptides are destinant publication probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may gene films is the amino acid sequence of a novel human secreted and
                                                                                                                                                                                                                                                                                                                                            New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 GATAGITTACCIGIGCAAATTACAGITCCGGAGAAAATACGGICAATAATAAAGGAAGGA 188
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Wood WI;
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4 LeuIrpLeu-----LeuLeuAladlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
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                                                                                                                                                                                                                                  Gerritsen ME, Goddard A, Godowski P.
Smith V, Stephan JF, Watanabe CK,
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Gaps:
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41.11%
31.79%
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N-PSDB; ACD68637.
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Grimaldi JC,
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42 SerGluileGluTyrGluGlnileSerTyrileIleProileAspGluLysLeuTyrThr 61 240 GTGAATTTAATGCAAAAAAACTTTTTACCCCATAATTTTAGAGTTTACAGTTATAGGC 299	300 ACAGGAATTATGAAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGTAT 359 81 GlnGlySerMetAanThrTvrSerSerAanIleGlnThrGlnCAfvrTvrGlnGlyAan 100	ATTGARGSTATCCAAAATCTGTGGTGATGGTTAGCACATGTACTGGACGGTA [] [] [] [] [] [] [] [] [] [] [] [] []		480 CATGTAATTTACCAAGTAAAACATAAAAGAAGCAGATGTTTCCTTATATAATGAGAAGGAT 539	540 ATTGAATCAAGAGATCTGTCCTTTAAATTACAAAGCGCAGAGCCACAGCAA 590 ::::::::::::::::::::::::::::::::::::	591 GATTITGCAAAGTATAAGAAATGCATGTTATAGTTGAAAACAATTGTATAAT 644 	645 CATATGGGGTCTGATACAACTGTTGCGCTCAAAAAGTTTTCCAGTTGATGGATTGACG 704 :::	705 AATGCTATTTTTGTTTCATTTACAATTATTCTGTCTTCATTGGAGCTTTGGATA 764 [  :::::	765 GATGAAAATATGCAACCACTGGAGAAGCTAATGAGTTATTACACACTTTTAAGA 824	825 TGGAAAACATCTTATCTTGTTTTACGTCCTCATGATGTGGCATTTTTACTTGTTACAGA 884			1005 CAATTATTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAATGCCAGTGCTCA 1064    :::    :::		•	1185 AATCAGCCTCGCTTAGATCCTTTTTCAAACAGCAAGGGAGGTGTGTGT	1245 GAAGCAGGAGAGAGTGTGACGGACTGAACAGGATTGTGCCCTTATTGGAGAAACA 1304 
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2058 GTAGCTATACCAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCATTCCAAA 2117
                                                                                                                                                                                                    1422 TGCGACCTCCCTGAATATTGCAATGGATCATCTGCCATCATGCCCAGAAAACCACTATGTT 1481
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1305 TGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGC 1364
                                                                                                   1365 TGCGAAAACTGTCTATTTATGTCAAAAGAAAGAATGTGTAGGCCT---TCCTTTGAAGAA 1421
                                                                                                                                    1482 CAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATGAGT 1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1602 TATICICACCTIAATICAAAGACTGATGTATCTGGAAACTGTGGTATAAGT---GATTCA 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1659 GGATACACACAGTGTGAAGCTGACAATCTGCAGTGCGGAAAATTAATATGTAAATATGTA 1718
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                          418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
                                                                                                                                                                                                                                  538 LysTyrValPheCysGlyTrpArgAsnLeulleCysGlyArgLeuValCysThrTyrPro 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    657 Ser-----LysGlyPheSerilePheProGluGluAspMetGlySerile----- 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 ------MetGluArgAlaSerGlyLysThr 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
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419

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945 GGAGGTGTTGTTCTGCACCCCAGAACCATAAGTCTGGAATCACTTGCAGTTATTTTAGCT 1004
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                                                                                                                                                                                                                                                        -----TCGCAGGCATCCTACAAATTGTAATTGAAGGGAAACCATATACT 239
                                                                                                      GIGAATITAAIGCAAAAAACTITITACCCCATAATITITAGAGTITACAGITATAGIGGC 299
                                                                                                                                                                      ACAGGAATTATGAAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTAT 359
                                                                                                                                                                                                    81 GlndiySerMetAsnThrTyrSerSerAspiledinThrGlndysTyrTyrdinGlyAsn 100
                                                                                                                                                                                                                                                                                                    CTACAGTTTGAAAATGTTAGTTATGGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAA 479
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| AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTrpSer 240
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361 SerCysSerLeuArgSerPheGlnAsnPhelleSerAsnValGlyValLysCysLeuGln 380
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62 ValHisLeuLysGlnArgTyrPheLeuAlaAgDAsnPheMetIleTyrLeuTyrAsn--- 80
     22 GlnAsnSerLeuLeuGlnIleValIleProGluLysIleGlnThrAsnThrAsnAspSer 41
                                                                    SerGlulleGluTyrGluGlnIleSerTyrIleIleProileAspGluLysLeuTyrThr
                                                                                                                                                                                                                                       ATTGAAGGTTATCCAAAATCTGTGGTGATGGTTAGCACATGTACTGGACTCAGGGGGGGTA
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                                       189 ATTGAA-
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                                                                                          Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthitis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATAGITTACCIGIGCAAAITACAGITCCGGAGAAAATACGGICAATAATAAAGGAAGGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGTGGGTCTTGTTTCTGCTCAGCGGGCTCGCGGGCTGCGGATGGAC---AGTAATTTT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PJ;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, ageralated macular degeneration, atherosclerosis, hypertension, arterial thrombophlebitis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, undur angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
                                                                 Novel human secreted and transmembrane protein PRO21340.
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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JC, Gurney
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GAAGCAGGAGAGGAGTGTGACTGTGGGACTGAACAGGATTGTGCCCTTATTGGAGAAACA 1304
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                                                                                                                TGCGAAAACTGTCTATTTATGTCAAAAGAAAGAATGTGTAGGCCT----TCCTTTGAAGAA 1421
                                                                                                                                                                         TGCGACCTCCCTGAATATTGCAATGGATCATCTGCATCATGCCCAGAAAACCACTATGTT 1481
                                                                                                                                                                                                                                1482 CAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATGAGT 1541
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CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
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ThrArgLy8ProPheHisGlnGluAsnGlyAspVallleTyrAlaPheValArgAspSer 577
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------MetGluArgAlaSerGlyLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProlleLeuIleVal-----
                           GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer
                                                        TGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGC
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The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TNF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation, the stimulation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
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Wood V
                                                                                                  PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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of a medicament for diagnosing or treating tumors or for measuring
detecting expression of an associated gene.
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Smith V, Stephan JF, Watanabe CK,
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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(first entry)
                                                      Human PRO21340 protein.
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Grimaldi JC, Gurney
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N-PSDB; ABT44270.
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06-NOV-2003
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ABJ72400 standard; protein; 787 AA.

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AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
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                                                                                                          ATTGAAGGTTATCCAAAATCTGTGTGATGGTTAGCACATGTACTGGACTCAGGGCGTA 419
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                                                      GAT-----TITGCAAAGTATATAGAAATGCATGTTATAGTTGAAAAACAATTGTATAAT
300 ACAGGAATTATGAAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumour in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention
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|SerGluIleGluTyrGluGlnIleSerTyrIleIleProIleAspGluLysLeuTyrThr
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                                                                                  ьки; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
tumour necrosis factor; proliferation; differentiation; gene therapy;
dermal fibroblast.
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                                                                                                                                                                                                                                                                                                                                                                                                                   New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence tumor in a mammal.
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Smith V, Stephan JF, Watanabe CK,
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29-JUN-2001; 2001WO-US021066.
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                                                                 Human PRO21340 protein
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N-PSDB; ABT44553
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418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
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| S18 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn
                                                        438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu
                                                                                                      1542 GGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTTGGCCCTTCAGAATGT
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ValCysileThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys
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The invention relates to an isolated nucleic acid encoding a PRO
polypeptide. Nucleic acids that encode PRO can be used to generate either
transganic animals or knock-out animals useful in developing and
creening of therapeutically useful reagents. The nucleic acids may also
be used in gene therapy for replacing defective gene, in chromosome
identification, as chromosome markers, or in generating probes to isolate
identification, TNP-alpha stimulation, human dermal fibroblasts stimulation
timulation, TNP-alpha stimulation, human dermal fibroblasts stimulation
chromosome
of the isolated nucleic acids may be used for recombinantly expressing
those markers. The PRO polypeptides and nucleic acids may also be used in
the isolated nucleic acids may be used for recombinantly expressing
those markers. The PRO polypeptides and nucleic acids may also be used in
tissue typing Anti-PRO antibodies are useful in diagnostic assays for
PRO and in affinity purification of PRO from recombinant cell culture or
natural sources. The present sequence represents the amino acid sequence
of a human secreted/transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 ATGIGGGTCTTGTTTCTGCTCAGGGGCTCGGGGCTGCGGATGGAC---AGTAATTTT 128
                                                                                                                                                                                                                                                                                                                                                        Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe
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                                                      therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
                                                                   fibroblast stimulation; tumour; tissue typing;
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                 Human secreted/transmembrane polypeptide PRO 21340.
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                                                 Human; chondrocyte stimulation; TNF-alpha
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                                                                                   affinity purification.
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ABO34295 standard; protein; 787

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C; Species: Macaca fascicularis (crab-eating macaque)
C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C; Accession: 602937; S55661
A; Ramarao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
B; Ramarao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
A; Ramarao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
A; Reference number: 612615
A; Residues: 1-735 cRAM>
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A; Residues: S55059; MUID:95260313; PMID:7741716
A; Residues: 1.722, S', 724-735 cPER>
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A; Cross-references: EMBL:X77653; NID:9794076; PIDN:CAA54733.1; PID:9794077
C; Superfamily: mouse meltrin alpha; disintegrin homology
F; 383-468/Domain: disintegrin homology cDIS>
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561 1809 581 1869 601 1989 641 2049 681	Db 701 ValLeuIleAlaileMetValLy8ValHi8FheGlnArgLy8Ly8TpArgThrGluAsp 720  Qy 2229 TATTCAAGCGATGAGCAACCTGAAAGTGAACCTAAAGGG 2273  Db 721 TyrSerThrAspGluGlnProGluSerGluSerGluBroLy8Gly 735  RESULT 3  \$47656  C,Species: Macaca fascicularis (crab-eating macaque)  C,Species: Macaca fascicularis (rab-eating macaque)  C,Species: Mulp: 943186664; PMID: 8043604  A,Reference number: S47656; MUID: 94318664; PMID: 80443604	A,Status; preliminary A,Robecule type: mRNA C,Superfamily: mouse meltrin alpha; disintegrin homology E,388-473/Domain: disintegrin homology <dis> Alignment Scores: Alignment Scores: 1.91e-94 Length: 756 Score: 1384.50 Matches: 296 Percent Similarity: 53.85\$ Conservative: 124 Bet Local Similarity: 29.94 Guery Match: 28.87\$ Indels: 66 DB:</dis>	US-10-054-683-18 (1-2640) x 847656 (1-756)  Oy

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A;Cross-references: UNIPROT:028482; EMBL:X76637; NID:g535016; PIDN:CAA54085.1; PID:g53501
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;392-477/Domain: disintegrin homology <DIS>
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84 LeuTyr---ValAspSerSerPheSerLysGlyHisCysPheTyrGlnGlyTyrValAla 102
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183 MetLeuSerLys------ArgThrLeuLysIle
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143 ValTyrArgIleLygA8nAspAlaIleGlyHisPheSerPheGlnGluAsnTyrProVal
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                                                                                                            transcript
RESULT 4
847645
twDC I protein - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_che
C;Accession: 847645 #sequence_revision 27-Jan-1995 #text_che
Biochim. Biophys. Acta 1218, 429-431, 1994
A;Title: Sequence and expression of a monkey testicular tran
A;Rocession: 84765
A;Status: preliminary
A;Molecule type: mRNA
A;Resiques: 1-736 cBRR>
                                                                                                                                                                                                                                                          736
281
145
270
69
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Matches:
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Best Local Similarity:
Query Match:
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|AlaAspGluIleLeuGlnArgPheLeuLeuTrpLyBGlnLyBLeuLeuPheGlnArgSer 271
                                                                                                                              CAAGGGAAGATGTGTGATGCAAACTATGCAGGAGGTGTTGTTCTGCACCCCCAGAACCATA 974
                                                                                                                                                                       312 ThrValGluAlaPheSerValValMetAlaGlnLeuLeuGly11eAsnLeuGlyLeuThr 331
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ValLeuGlnProGluLeuLysCysPheGlnAspLysThrIleSerGluMetThrTyrGln 391
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ThrSerGluPheCysValProAspValLysAlaAlaAspLeuGluTyrCysSerAsnLys 489
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                                            CATGATGTGGCATTTTTACTTGTTACAGAGAAAAGTCAAATTATGTTGGTGCAACCTTT
                                 ATTATTCTGTCTTCATTGGAGCTTTGGATAGATGAAAATAAAATTGCAACCACTGGAGAA
                                                                         GCTAATGAGTTATTACACACATTTTTAAGATGGAAAACATCTTATCTTGTTTTACGTCCT
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cyritestin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Daccies: O-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 184784; S18968
R;Senftleben, A.; Wallat, S.; Lemaire, L.; Heinlein, U.A.O.
Dev. Growth Differ: 36, 49-88, 1994
A;Title: Pre and postmeiotic germ cell specific expression of TAZ83, a gene encoding a px
                                                        1868
                                                                                                                                                                                                                                                                     TGCAATGATAGAGGTGTATGCAATAACAAAAGCACTGTCACTGTAGTGCTTCATATTA 1988
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|||||||||CysArgGlyCysArgTyrLeuSerGluLeuAsnIleThrLysCysThrThrAsn
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                                                   CATGCAGACAGCCAAAAGATGTGGATAAAAGATGGAACTTCTTGTGGTTCAAATAAGGTT
                                                                                                         AlaSerLysGlnLeuGlyThrTyrThrGluAspIleThrAlaCysGlyGlnGlnLysVal
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A,Residues: 1-623 <RES>
A,Cross-references: UNIPROT:Q62287; EMBL:X64227; NID:g54264; PID:g54265
C,Genetics:
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C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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385 Se	1245 GAJ 	1305 TG	423 Cy	1365 TG 	1419 GA	463 GI	1479 GT	483 Ala	1539 AG	503 AB	1596 GAV	1656 TC		1716 GT	556 A81	1776 CA	576 Gl	1836 AAJ	596 His	1896 TC	616 His	1947 TG(	636 Cyr	2007 CAJ 656 Th	2067 CCJ	675 Se	2127 TG	693 Ile	2187 GT	709 Ala	2247 CC	729 His
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:::	ATTGAATCGCAGGCATCCTACAAAATTGTAATTGAAGGGAACCATATACTGTGAATTTA	45 AIGGIABBABABCHUTHTIYEVAIVAITHTILEGIUGLYLYBALATYTTHTLEUGINLEU 64 249 ATGGIABABABCHUTHTHTAGGGGATABATHTTAGAGTTTAGGGGTATAAGAGGGAAGAGAAAGAAAAAAA		309 ATGAAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTATATTGAAGGT 368		369 TATCCAAAICTGTGGTGATGGTTAGGACTGTACTGGACTGAGGGGGTACTACAGTTT 428	いい はんかい かんかん かんかん かんかん かんかん かんかん かんかん かん		489 TACCAAGTAAAACATAAGAAAGCAGATGTTTCGTTATATAAT 530	145 TyrGlulleLysAsnAsnLysIleAspTyrSerProLeuLysGluAsnPheAlaAsnSer 164	531 GAGAAGGATATTGAATCAAGAGATCTGTCCTTTAAATTACAAAGCGCAGAGCCACAGCAA 590	165 GlüdlnGlüSerGlüSerTyrArglleLeuValLysProGlüLysGlySerAsnSerThr 184	GATTTTGCAAAGTATATAGAAATGCATGTTATAGTTGAAAACAATTGTATAATCATATG		651 GGGTCTGATACAACTGTTGTCGCTCAAAAGTTTTCCAGTTGATTGGATTGACGAATGCT 710 205 GLOGACGTLY	ATTHEMPTOREMED BEFORE A BEFORE ATTREMPTOREMED AND ATTREMPTOREMED BEFORE A BEFORE A STATE AND A PART	### WELPHESETGING ### WELPHESETGING ###################################			831 ACATCTTATCTTGTTTTACGTCCTCATGATGTGGCATTTTTACTTGTTTACAGAGAAAG 890	::: :: ::: ::: ::: ::: ::: ::: ::: :::			951 GTTGTTCTGCACCCCCAGAACCATAAGTCTGGAATCACTTGCAGTTATTTTAGCTCAATTA 1010	305 IleAlaLeuHisProLysThrLeuAlaValGluGlyPheAlaIleValLeuSerGlnLeu 324	TTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAAATGCCAGTGCTCAGGAGCT	LeuGLY11eABhLeuGlYLeuAlaTYrABpABpValTYrABnCYBPheCYBPrOGLYSer	10/1 GICIOCAITAIGAAICCAGAACCAATICATIICAGGGGGGGGGGG	AGCTTCCAAGACTTTTGCAACTATTTTATTTCAAATTTCAAAACCAGAAGAACTCCAAAATTTCAAAATTTTATTATTATTATTATTATT		1191 CCTCGCTTAGATCCTTTTTCAAACAGCAAGCAGTGTGTGGTAATGCAAAGCTG 1244	
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TCAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATG 1538 ATCTCTGCATTGCTGTGGAATTTGCCAGTGATCATGCAGACAGCCAAAAGATGTGGATA 1835 ATCAGATCTATGGCCTGGTGGGAGTATTGACAGTGGCAATTTTCCACCTGTAGCTATA 2066 PAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCATTCCAAACCAATGAGA 2126 IGAAAGTTAATTTCCAAAGGAAAAATGGAGAACTGAGGACTATTCAAGCGATGAGCAA 2246 AGCAGGAGAGGAGTGTGACTGTGGGACTGAACAGGATTGTGCCCTTATTGGAGAAACA 1304 AATGITATTCTCACCTTAATTCAAAGACTGATGTATCTGGAAACTGTGGTATAAGTGAT 1655 AAGATGGAACTTCTTGTGGTTCAAATAAGGTTTGCAGGAATCAAAGATGTGTGAGTTCT 1895 CATACTIG-----GGTTATGATIGT---ACTACTGACAAAIGCAATGATAGAGGIGTA 1946 SCANTAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCAGATTGCTCAGTT 2006 3GCCATITITICITATICATICCITICITITATIATITICIGIGIACIGATIGCIATAAIG 2186 SCIGIGATATIGCCACATGIAGATITAAAGCCGGITCAAACIGIGCTGAAGGACCAIGC 1364 yscysdsnprolysdspCysThrLeuIledspAlaAlaGlnCysGlyThrGlyProCys 442 ||::: ysAspiysArgThrCysThrIleAlaGluArgGlyArgLeuCysArgIysSsrLysAsp 462 aAlaAspLeuGluProCysAsnAsnGluThrAlaTyrCysPheGlyGlyValCysArg 502 alCysAlaGluValAsnLeuGlnAsnAspLysPheGlyAsnCys----- 537 snPheAlaGluValIleGlnThrGluLysTyrAspValGlnTyrThrTyrLeuGlydly 575 :::|||:::::: |nvalCysValSerAlaHisLeuArgSerGlnThrGlyThrArgAspAspThrTyrVal 595 ||||||||| ||||||||| :::||||||| isAspGlyThrValCysGlySerGlyGlnValCysPheArgGlyAspCysLeuArgVal 615 |||:::::: :::|||||| :::::: |eserPheTyrIleLeuLeuProPheLeuValVal-------LeuAlaPheMet 708 |||| :::|||::: |:ThrProLeullePheLysArgHis-----GlyLeuLysTyrLysLysUslLeuLeu 692 srGluThrGluPheValValGlnProGlnGlyGlySerTyrCysGlyAsnHisLeuLeu 404 CTGAAAGTGAGAGTGAACCTAAAGGG 2273 isiyeGluGluAlaPheAsnArgGly 737

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SerMetAspAsnPheLysTyrPheAlaSerGlnTyrGlyLeuThrCysLeuArgAsnThr 381
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242 AsnLysValThrAsnThrArgArgProAspAspAspLeuPheArgPheSerAspTrpLys
                                                                                                                                                                                    262 ArglysHisValSerLeulysSerHisTyrValAlaTyrLeuLeuThrPheAspLysTyr
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460 ValaspLysAspPheAspPheAspGluTyrCysAsnGlyArgSerGlyAspCysValHis
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202 GlySerAspIleLysThrValThrGlnLysIleIleGlnValIleGlyLeuValAsnAla
                                                                                                   AATAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACACACATTTTAAGATGGAAA
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                                                ADAM 5 protein precursor - guinea pig
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Date: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 148100
R; Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D. Dev. Biol. 169, 378-383, 1995
A; Title: ADAM, a widely distributed and developmentally regulated gene family encoding m A; Reference number: 148100
A; MulD:95269891; PMID:7750654
A; Accession: 148100
A; MulD:9526981; PMID:7750654
A; Accession: Ive: mRNA
A; Statuus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-777 cRES>
A; Cross-references: UNIPROT:Q60472; EMBL:U22060; NID:9965005; PIDN:AAA74918.1; PID:99650
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C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>
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Conservative:
Mismatches:
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PheValllePheSerValLeuValAlaThrValValLy8ValTyrTyrGlnLy8Ly8Ly8 331
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ProValTyrArgSerAsnProValCysGlyAsnAsnArgValGluGlnGlyGluAspCys
                                 CCTTTTTCAAACAGCAAGCAGTGTGTGTAATGCAAAGCTGGAAGCAGGAGAGGGGTGT
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C,Species: Cavia porcellus (guinea pig)
C,Species: Cavia porcellus (guinea pig)
C,Date: 29-Jan-1993 #sequence_revieton 29-Jan-1993 #text_change 09-Jun-2000
C,Accession: S23403; S25696
R,Blobel, C.P.; Wolfsberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
Nature 356, 248-252, 1992
A,Title: A potential fusion peptide and an integrin ligand domain in a protein active in A;Reference number: S23403; MUD:92204234; PMID:1552944
A,Accession: S23403
A,Molecule type: mRNA
A,Residues: 1-357 < BLO1>
A,Gross-references: EMBL:211720
A,Cross-references: EMBL:211720
A,Cross-references: EMBL:211720
A,Cross-references: EMBL:211720
A,Cross-references: EMBL:211720
A,Cross-references: EMBL:211720
A,Molecule type: protein
A,Residues: 5-8, X, 10-12;67-88;125-129, X, 131-134, X, 136-141, X, 143;154, X, 156-161;
C,Superfamily: mouse meltrin alpha; disintegrin homology
C,Rewords: glycoprotein; transmembrane protein
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F;5-37/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>
F;5-37/Product: sperm uniface protein homology <CK-BY/Domain: disintegrin homology covalent; #status predicted
F;303-323/Domain: transmembrane #status predicted <TWM>
F;78,186,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                    :::||||:::||| ::: || ArgAspAspIleCysValAraThrThrLysThrValArgLysIleIleArgAspLeuSer 594
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C:Comment: This protein, which is a member of the a disintegrin and metalloprotease
lular functions. It is proteolytically active, and has an alpha-secretase activity f
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180 TyrSerIleGluProMetAspSerSerArgÀrgPheGluHisValLeuTyrThrMetAla 199 501 CATAAGAAAGCAGATGTTTCCTTATATAATGAGAAGGATATTGAATCAAGAGAT 554	555CTGTCCTTTAAATTACAAAGGCGAGAGCCACAGGAA 590     :::::     :::     215 ValValSerThrSerTrpGlnGlnGlnGlnGlnGlnGlnGlnGlySerArgLy8PrOHisAspLeuGlnAlaLeuSer 234	591GATTTTGCAAAGTATATAGAAATGCATGTTATAGTTGAAAAACAATTGTAT 641 	642 AATCATATGGGGTCTGATACAACTGTTGTCGCTCAAAAGTTTTCCAGTTGATTGGATTG 701	702 ACGAAIGCTAITTIGTTICAITIAAIATIACAATIATICIGICTICAITGGAGCTITIGG 761 	762 ATAGATGAAAATTTGCAACCACTGGAGAAGCTAATGAGTTATTACACACATTTTA 821	822 AGATGGAAACATCTTGTTTTACGTCCTCATGATGTGGCATTTTTACTTGTT 878        ::::	879 TACAGAGAAAAGTCAAATTATGTTGGTGCAACCTTTCAAGGGAAGATGTGTGATGCAAAC 938 335 GlyHisHisProGlyGlnAsnThrdlyGlnAlaPheLeuSerGlyAlaCysSerSerGly 354	939 TATGCAGGAGGTGTTGTTCTGCACCCCGAAACCATAAGTCTGGAATCACTTGCAGTT 995 355 PheAlaAlaAlaValGluSerPheHisHisGluAspMetLeuLeuPheAlaAla 372	996 ATTTTAGCTCAATTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAAATGC 1055	1056 CAGIGCTCAGGAGCTGTCTGCATTATGAATCCAGAAGCAATTCATTC			1233 AATGCAAAGCTGGAAGGAGGAGTGTGACTGTGGGACTGAACAGGATTGTGCCCTT 1292 	1293 ATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCT 1352 :::	1353 GAAGGACCATGCTGAAAACTGTCTATTTATGTCAAAAGAAAG	1413 TTTGAAGAATGCGACCTCCCTGAATATTGCAATGGATCATCTGCATCATGCACAGAAAAC 1472 :::	1473 CACTATGTTCAGACTGGGCATCCGTGTGGACTGAATGGATCTGTATAGATGGAGTT 1532 
8 & 8	cy Dp	දි සි	S G	S G	ò q	o S	Š d	ço q	ò q	5 B 6	3 A	දි දි	රි පි	& 8	δ <sup>α</sup>	S G	<b>ራ</b> ዋ  .
Db 557 GlyAsnGluTyrLysLysCysAlaThrGlyAsnAlaLeuCysGlyLysLeuGlnCysGlu 576  Qy 1713 TATGTAGGTAAATTTTATTACAAATTCCAAGAGCCACTATTATTATTATGCCAACATAAGT 1772	OY 1773GGACATCTCTGCATTGCTGTGGAATTTGCCAGTGATCATGCA 1814	Qy 1815 GACAGCCAAAAGATGTGGATAAAAGACTTCTTGTGGTTCAAATAAGGTTTGCAGG 1874	Qy     1875 AATCAAAGATGTGTGAGTTCTTCATACTTGGGTTATGATTGTACTACTGACAAATGC 1931             :::	Oy 1932 AATGATAGAGGT 1943  Db 651 HisGlyHisGly 654	RESULT 9 S55060 fertilin alpha-II - crab-eating macaque	C;Species: Macaca fascicularis (crab-eating macaque) C;Bate: 23-Mug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C;Accession: S55660 R;Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.	Biochem. J. 307, 843-850, 1995 A,Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms. A,Reference number: S55059; MUID:95260313; PMID:7741716 A,Accession: S55060	A;Status: preliminary A;Molecule type: mRNA A;Residus: 1-825 <per> A;Cross-references: UNIPROT:Q28477; EMBL:X79809; NID:g794074; PIDN:CAA56204.1; PID:g794C</per>	C;Superfamily: mouse meltrin alpha; disintegrin homology F;443-523/Domain: disintegrin homology <dis> F;377/Active site: Glu #status predicted</dis>	Alignment Scores:  Pred. No.: 1.69e-68 Length: 825 Score: 1033.50 Matches: 257 Percent Similarity: 48.51\$ Conservative: 117 Best Local Similarity: 33.33\$ Mismatches: 310	S-10-054-683-18 (1-2640) x S55060 (1-825)	Oy 144 CAAATTACAGTTCCGGAGAAAATACGGTCAATAATAAAGGAAGG	TCCTACAAAATTGTAATTGAAGGAAACCATATACTGTGAATTTAATGCAAAAAAC THIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	261 TTTTACCCCATAATTTAGAGTTTACAGTTATAGTGGCACAGGAATTATGAAACCACTT ::	121 HIBFNEVALABNABHRNEFICVALIJISERIJIHBSABNGLYILEEGGUSIJVALNGIL  321 GACCAAGATTTCAGAATTTCTGCCACTACCAAGGTATATTGAAGGTTATCCAAAATCT  140 SerprophelleSerHistanCveHistVcGluGluTvTlGdluGlvValSerGluSe	381 GTGGTGATGGTTAGCACATGTACTGGACTCAGGGGGGTACAGGTTTGAAAATGTTAGT 160 Pheval Servial Asmith's Color of the color	441 TATGGAATAGAACCCCTGGAGTCTTCAGTTGGATTTGAACATGTAACTATACCAAGTAAAA 50

Qy       1533 TGTATGAGTGGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTTGGCCCT       1592	A;Molecule type: mRNA A;Residues: 1-905 <per> A;Cross-references: UNIPROT:Q28476; EMBL:X79808; NID:g794072; PIDN:CAA56203.1; PID:g7940' C;Superfamily: mouse meltrin alpha; disintegrin homology F:442-522/Domain: disintegrin homology <dis> F;376/Active site: Glu #status predicted</dis></per>
Db 563 GluAspCysfYrIleSerMerAsnThrArgGlyAspArgPheGlYAshCysGlYHisPro 582  Qy 1647ATAAGTGATTCAGGATACACACAGTGTGAACACTGCACACACA	Alignment Scores: 1.1e-67 Length: 905  Pred. No.: 1022.50 Matches: 250  Percent Similarity: 50.07* Conservative: 123  Best Local Similarity: 33.56* Mismatches: 297  Query Match: 21.32* Indels: 75  DB: 2 Gaps: 29  US-10-054-683-18 (1-2640) x S55059 (1-905)
Qy 1752 ATTATTTATGCCAACATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGT 1805 :::	<pre>Qy 135 TTACCTGTGCAAATTACAGTTCCGGAGAAATACGGTCAATAAAAAGGAAGG</pre>
Qy 1806 GATCATGCAGACACCAAAAGATGTGGATAAAAGATGGAACTTCTTGTGGTTCAAATAAG 1865 	Qy 195 TCGCAGGCATCCTACAAAATTGTAATTGAAGGGAAACCATATACTGTGAATTTAATG 251
Qy 1866 GTTTGCAGGAATCAAAGATGTGTGAGTTCTTCATACTTGGGTTATGATTGTACTACTGAC 1925	Qy 252 CAAAAAAACTTTTTACCCCATAATTTTAGAGTTTACAGTATATAGTGGCACAGGAATTATG 311 117 in::::::::::::::::::::::::::::::::::::
OY 1926 AAAIGCAATGATAGAGGTGTATGCAATAACAAAAGCACTGTCACTGTAGTGCTTCA 1982 :::	Qy 312 AAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTATATTGAAGGTTAT 371 512 AAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTATATTGAAGGTTAT 371 512 BAACCACTTGAAGAATTTTCAGAATTTCTGCCACTACCAAGGGTATATTAGAAGGTTAT 371 513 AAACCACTTGACCAAGAATTTCTGCCACTACCAAGGGTATATTAGAAGGTATATTAGAAGGTAAAGAAG
Qy 1983 TATTIACCTCCAGAITGCTCAGITCAATCAGATCTAIGGCTGGTGGGAGTAITGACAGI 2042 :::	Oy 372 CCAAAATCTGTGGTGATGGTTÄGCACATGTACTGGACTCAGGGGGGGGTACTACAAA 431 
OY 2043 GCCAATTTTCCACCTGTAGCTATACCAGCCAGACTCCCTGAAAGGCGCTACATT 2096	Qy 432 AATGTTAGGTAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAACATGTAATTTAC 491
Qy 2097 GAGAACATTTACCAAACCAATGAGA	Qy 492 CAAGTAAAACATAAGAAAGCAGATGTTTCCTTATATAATGAGAATATTGAATCAAGA 551
Qy 2127TGGCCATTTTCTTATTCATTCTTTATTATTTTCTGTGTACTGATT 2177	Oy 552 GAT STGTCCTTTAAATTACAAAGCGCAGAGCCACAGCAA 590
Qy 2178 GCTATAATGGTGAAAGTTAATTTCCAAAGGAAAAATGGAGAACTGAG 2225	Qy 591GATTTTGCAAAGTATATAGAAATGCATGTTATAGAAAA 632       ::           ::    
Qy 2226 GACTATTCAAGCGATGAGCAACCTGAA	Qy 633 CAATTGTATAATCATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTCCAGTTG 692     :::
Oy 2253AGTGAGAGTGAACCTAAAGGGTAGTCTGGA 2282	Qy 693 ATIGGATIGAATGCTATITIGTITCATITAATATIACAATTATCTGTCTTCATIG 752
RESULT 10 S55059 fertilin alpha-I - crab-eating macaque C;Species: Macaca fascicularis (crab-eating macaque) C;Species: Macaca fascicularis (crab-eating macaque) C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C;Accession: S55059 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C;Accession: S55059 #0.; Jones, R.; Hall, L. Biochem. J. 307, 843-850, 1995 A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms. A;Reference number: S55059; MUID:95260313; PMID:7741716 A;Status: preliminary	Oy 753 GAGCTTTGGATAGATGAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACAC 812

	8 8	2		o S	2 &		8	DD RESULT 11	S71949 metallopro	C;Species: C;Date: 19	C, Accessic R, McKie, N	A;Title: CA; A;Reference	A; Accessio A; Status:	A;Molecule A;Residues A;Cross-re	A;Experime R;McKie, N	A;Title: E	A; Status:	A; Residues	A;Experime C;Function A;Descript	A, Note: me C, Superfam	C; Keywords F;1-24/Dom	F;295-000/E F;295-378/	F;574-598/ F;622-642/	F;57,229,2 F;229,233, F;230/Acti	Alignment	Pred. No.: Score:	Best Local Query Mato	DB:	US-10-054-
930 GATGCAAACTATGCAGGAGGTGTTGTTCTGCACCCCAGAACCATAAGTCTGGAATCA 986 351 SerSerGlyPhealaAlaAlaAlaAlaValGluSerPheHi8Hi8GluAspMetLeuLeu 368	987 CTTGCAGTTATTTAGCTCCAATTATTGAGCCTTAGTATGAGGGATCACTTATGATGACATT 1046	PheAlaAlaLeuMetValHisGluLeuGlyHisAsnLeuGlyIleGlnHisAspHis	1047 Archanicality 11051cAccarcity 1Alicality 1105	1104 AGTGGTGTGAAGATCTTTAGTAACTGCAGCTTTGGAGACTTTTGCACATTTTATTTCAAAG 1163	408 SerGlyPheSerAsnCysSerSerTspPheHisGlnPheLeuArgGlu 424	1164 CAGAAGTCCCAGTGTCTTCACAATCAGCCTCGCTTAGATCCTTTTTTCAAACAGCAAGCA	1224 GTGTGGTAATGCAAAGCTGGAAGCAGAGGAGGAGTGTGACTGTGACTGGAACTGAACAGAT 1283	445 AlaCysGlyAsnGlyValValGluAspThrGluGluCysAspCysGlySerAla 462	1284 TGTGCCCTTATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCA 1343	AACTGTGCTGAAGGACCATGCTGCTATTTATGTCAAAAGAAAG		AGGCCTTCCTTTGAAGAATGCGACCTCCCTGAATATTGCAATGATGATCATGTCTGCATCATGT	ArgProThrGlnAspGluCysAspLeuProGluTyrCysAspGlySerSerAlaGluCys	1464 CCAGAAAACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATA 1523 	1524 GATGGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAG 1583	539 GlyGlnCygLysAsnProAspAsnGlnCysValAsnIleTyrGlyTyrProAlaArg 558	TTTGGCCCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTGGAAACTGT	SerAlaProGluAspCysTyrIleSerMetAsnThrArgGlyAspArgPheGlyAsnCys	1644 GGTATAAGTGATTCAGGATACACACAGTGAGTGAGAGTGAGATGC 1694 			1749ACTATTATTATGCCAACATAAGTGGACATCTCTGCATTGCTGTGGAATTT 1799	615 GlnHisThrVallleGlnValProHisAspAsnAspTrpCysTrpSerMetAspAlaAsp 634	1800GCCAGTGATCATGCAGACAGCCAAAAGATGGGATAAAAGATGGAACTTCTTGTGGT 1856	TCAAATAAGGTTTGCAGGAATCAAAGATGTGAGTTCTTCATACTTGGGTTATGTTGT	ProAsnLysValCysThrAspTyrSerCysValHisHisSer1leLeuLeuTyrAspCys	1917 ACTACTGACAAATGCAATGATAGAGGTGTATGCAATAACAAAAAGGACTGTCACTGT 1973		1974 AGTGCTTCATATTTACCTCCAGATTGCTCAGTTCAATCAGATCTATGGCCTGGTGGGAGT 2033
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references: UNIPROT:Q13443
nental source: myeloma cells
N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,
Biophys. Res. Commun. 230, 335-339, 1997
Expression of members of a novel membrane linked metalloproteinase family (ADAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ate names: disintegrin 12; myeloma cell metalloproteinase MCMP s: Homo sapiens (man) son: S71949; PC4264 sion: S71949; Mullised metalloproteinase from human myeloma cells. Cloning of a novel membrane-linked metalloproteinase from human myeloma cells. nor s71949; Mullised Metalloproteinase from human myeloma cells. S71949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                  2094 ATTGAGAACATTTACCATTCCAAACCAATGAGATGGCCA--------TTTTTC 2138
                                                               2139 TTATTCATTCCTTTCTTATTATTTCTGTGTACTGATTGCTATAATGGTGAAGTTAAT 2198
                                                                                                                                                                                                                                                                                                                  2199 TTCCAAAGGAAAAATGGAGAACT------GAGGACTATTCAAGCGATGAG 2243
                                                                                           :::||||||||||
710 ValAspSerGly------ProProGlyMetGlnValThrAsnAsnSerGluSerGly 726
                                                                                                                                                                          |||:::|||
727 SerGluSerIleAlaArgGlyGlnSerLeuArgGlnAspValAspTyrLysLeuValVal 746
::: :::||| |||:::::| ||| 375 TyrLeuCysSerGluValGluThrAlaValAlaGluValGluGluSerSerThrGluThr 784
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                         2244 CAACCTGAAAGTGAG 2258
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785 ThrLeuGluSerGlu 789
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al Similarity:
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C;Species: Mis musculus (house mouse)
C;Species: 10-Apr-1996 #text_change 09-Jul-2004
C;Date: 10-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60257
R;Yagami-Hiromasa, T.; Sato, T.; Kurisaki, T.; Kamijo, K.; Nabeshima, Y.I.; Fujisawa-Sehi Nature 377, 652-656, 1995
A;Title: A metalloprotease-disintegrin participating in myoblast fusion.
A;Reference number: S60257; MUID:96026308; PMID:7566181
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                                                                                                                                                                                                           1587 GGCCCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTGGAAACTGTGGT 1646
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                                                                                                                                       GGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTT 1586
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1407 CCTTCCTTTGAAGAATGCGACCTCCCTGAATATTGCAATGGATCATCTGCATCATGATGTGTCA 1466
                                                                     GAAAACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATAGAT 1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTAATATGTAAATATGTAGGTAAATTTTTATTACAAATTCCAAGAGCCACTATTATT 1757
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                       GlyLysThrSerGluCysAspValProGluTyrCysAsnGlySerSerGlnPheCysGln
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A; Residues: 1-903 < YAG>
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| AspCysGlyGluProGluGluCysThr-----AsnArgCysCysAsnAlaThrThr 453
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LygAsnCysHisCysGluAlaHisTrpAlaProProPheCys-----AspLysPhe 688
|||| ::: ::: ||| ||| ||| AppthrLeugluArgGlyCysSerCysArgMetAlaAlaGluLysGlyGlyCysIleMet 378
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404 LysLeuValCysThrAspValArgTyrLeuProLysValLysProLeuHisSerLeuLeu
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                           230 ArgGlyAlaCysLeuLeuAspGluProGlyArgGlnSerArgMetArgArgAlaAlaAsn
                                                             TGTGGTAATGCAAAGCTGGAAGCAGAGAGGAGTGTGACTGTGGGACTGAACAGGATTGT
                                                                              287 GCCCTTATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAAC
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                                                                Primakoff, P.; Myles,
fertilin alpha precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacession: 149281
R;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; M.
Dev. Biol. 169, 378-383, 1995
A;Title: ADAM, a widely distributed and developmentally regulated gene family en A;Reference number: 148100; MUID:95269891; PMID:7750654
A;Reference number: 149281
A;Reference number: L49281
A;Reference number: L49281
A;Reference number: L40281
A;Reference number: L40281
A;Residues: 1-600 - RES
A;Cross-references: EMBL:U22056; NID:9965009; PIDN:AAA74920.1; PID:9965010
C;Genetics: ADAM I
C;Superfamily: disintegrin homology
E;246-256/Domain: disintegrin homology
E;246-256/Domain: disintegrin homology
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HisalavalTyrLysTyr	217 AspLeuAspLysileLysThrArgMetTyrGluIleValAsnThrValAsnGluijeTyr 236 717 GTTTCATTTAATATTACAATTATTCTGCTTTCGGGGCTTTGGATAGATGAAAATAAAA 718 GTTTCATTTAAATATTACAATTATTCTGCTTTCATTGGACTTTGGATAGATGAAAAAAAA	AGCCTTAGGAGATCACTTATGATGACATTAACAAATGCCAGTGCTCTCTTAGTATGGAGATCTTTAGTAACTGCTCTCTTAGTAACTGCAGAGCTGTCTTAGTAACTGCAGAGCTGTCTTAGTAACTGCAGAGCTGTTAGTAACTGCAGAGATTATGAACTGCAGAGATTATATATA
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1614 AATICAAAGACIGAIGIAICIGGAAACIGIGGIAIAAGIGAIICAGGAIACACACAGIGI 1673
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MEDLINE=97224507; PubMed=9070941;
Burkin H.R., Burkin D.J., Davey P.M., Griffin D.K., Affara N.A.;
"Mapping, sequence, and expression analysis of the human fertilin beta
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Gupte S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F.;
"Molecular cloning of the human fertilin beta subunit.";
Biochem. Biophys. Res. Commun. 224:318-326(1996).
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MEDLINE=97193554; PubMed=9041139;
Vidaeus C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows
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099965; P78326; Q9UQQ8;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain (Fertilin beta subunit, (FH-30) (PH30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The strill in beta: identification, characterization, and chromosomal mapping of an ADAM gene family member."; Mol. Reprod. Dev. 46:363-369(1997).
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AD1A_MOUSE
AD01_RAT
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Q28482
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AD09 HUMAN
Q60816
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AD09_MOUSE
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 NCBI_TaxID=9606;
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-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=0.1 -LGOPEL=0 -LGOPEXT=0
-DB=UniProt_02 -QEMT=fastan -SUPFIX=n2p.rup -MINMATCH=0.1 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DGCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-UOTFWHEPAD-NORMMEAXT -HEAPSIZEE=500 -MINLEN=0 -MAXEN=2000000000
-USER=US10054683 @CGN 1 1 518 @runat 10012005 174510 15496 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Q69290 homo sapien

A8464547 homo sapien

Q86688 sus scrofa

Q77780 bos taurus

Q28660 oryccolagus

Q6302 rattus norv

Q60718 mus musculu

Q60411 cavia porce

Q95194 macaca fasc

Q95194 homo sapien

Q8tc27 homo sapien
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Q8tc42 homo sapien
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Copyright (c) 1993 - 2005 Compugen Ltd.
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DR InterPro; 1FR001502; PEPTidase M12B.

DR InterPro; 1FR001502; Peptidase M12B.

DR InterPro; 1FR001502; Peptidase M12B.

DR InterPro; 1FR001602; Peptidase M12B.

DR InterPro; 1FR001602; Peptidase M12B.

DR Pfam; PF001201; Disintegrin; 1.

DR PFAM; PF00142; Reprolysin; 1.

DR PRINTS; PR001604; Disintegrin; 1.

DR PRINTS; PR001604; Disintegrin; 1.

DR SWART; SW00608; ACR; 1.

DR SWART; SW00608; DISINFEGRIN; 1.

DR SWART; SW00608; DISINFEGRIN; 1.

DR SWART; SW001608; DISINFEGRIN; 1.

DR PROSITE; PS501215; ADAM MEPRO; 1.

DR PROSITE; PS501215; DISINFEGRIN; 1; 1.

DR PROSITE; PS00129; EGF 1; FALSE NEG.

W Alternative splicing; Cell adhesion; EGF-like domain; Glycoprotein;

W Signal; Transmembrane.

TH PROPER 17 174

PROPER 17 174

PROPER 17 175 735 ADAM 2.
                       GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005178; F:integrin binding; TAS.
GO; GO:0008237; F:metallopeptidase activity; TAS.
GO; GO:000342; P:fusion of sperm to egg plasma membrane; TAS.
InterPro; IPR006586; ADAM cysteine.
InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
Metalloprotease-like.
Disintegrin-like.
Cys-rich.
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92867B5340BEE01F CRC64;
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By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC.)
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V -> G (in Ref. 3).
V -> G (in Ref. 3).
D -> H (in Ref. 1).
I -> T (in Ref. 1).
G -> S (in Ref. 1).
G -> S (in Ref. 3).
G -> S (in Ref. 3).
S -> G (in Ref. 3).
N -> D (in Ref. 3).
N -> D (in Ref. 3).
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Matches:
Conservative:
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Indels:
Gaps:
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Best Local Similarity:
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Pred. No.:
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     TISSUE=Testis,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Altausner R.D. Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altausner R.D., Collins F.S., Wagner L., Scheefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

A HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Lodgelland N.A., Parmer A.A., Rubin G.M., Hong L.,

Black C. M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rahla S.S., Lodgellando N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schwutz S., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

And Monian and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall L., Frayne J.; "Nucleotide sequence of the human fertilin beta transcript."; Submitted (AFR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q99965-1; Sequence=Displayed;
                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
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EMBL; X99374; CAA67753.1; -...
EMBL; AJ133005; CAB40813.1; -...
EMBL; AJ13405; CAB40813.1; -...
PIRJ; UC4861; JC4861.1; -...
HSSP; P30403; IN4Y.
TISSUE=Testis;
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Name=1

+

(Potential) (Potential)

(in isoform ip\_005471.

(in Ref.

HSSP; P30403; 1N4Y. MEROPS; M12.950; -. Genew; HGNC:198; ADAM2.

US-10-(	US-10-054-683-18 (1-2640) x AD02_HUMAN (1-735)	q <sub>0</sub>	1 GlualaileHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAla 360
රු සි	72 ATGTGGGTCTTGTTTCTGCTCAGCGGCTCGGCGGCTGCGGACAGTAATTTT 128 	<b>&amp;</b> 8	38
දු පු	GATAGTTTACCTGTGCAAATTACAGTTCCGGAGAAAATACGGTCAATAATAAGGAAGG	<i>&amp;</i> 8	9 TTCAAACAGCAAGGAGTGGTAATGCAAAGCTGGAAGCAGAAGAGAGAG
<u>ک</u> 8		<b>&amp;</b> 8	9 GGGACTGAACAGGATTGTGCCCTTATTGGAGAACATGCTGTGATATTGCCACATGTTAGA 132: 
දි සි	SAATT	<i>≿</i> 8	9 TTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGCGAAAACTGTCTATTTATGTCA 138 
දු පු	309 ATGAAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTATATTGAAGGT 368	<i>&amp;</i> 8	9 AAAGAAAGAATGTGTAGGCCTTCCTTTGAAGAATGCGACCTCCCTGAATATTGCAATGGA 144( 
è 8	369 TATCCAAAATCTGTGGTGATTAGCACATGTACTGGACTCAGGGCGTACTACAGTTT 428 	& 8 	<b>ч</b>
ර සි	GAAARGTTAGTAAGAATAGAACCCTGGAGTCTTCAGTTGGACTTTGAAATT	& 8	9 CAATGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACTTT 156 
රු සි	TACCAAGTAAAACATAAGAAAGCACATGTTTCCTTATATAATGAAGGATATTGAATCA 5	& g	1569 GGCAAAGAAGTATGGCCCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGAT 1628 
8 8 8	AGAGATCHCTCCTTTAAATTACAAAGCGAGAGCCACAGCACAG	è a	1629 GTATCTGGAAACTGTGGTATAAGTGATTCAGGATACACACAGTGTGAAGCTGACAATCTG 1688 
් ර සි	GAATGCATGTTATAGTTGAAAACAATTGTATAATCATATATGGGGTCTGATACAACGTTGTT	ò 9	1689 CAGTGCGGAAATTAATATGTAAATATGTAGGTAAATTTTTATTACAAATTCCAAGAGCC 1748 
1 & A	GTCGCTCAAAAAGTTTTCCAGTTGATTGATTGACGATGCTATTTTTGTTTAAT	ò a	1749 ACTATTATTATGCCAACATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGTGAT 1808 
k & 8	ATTACAATTATCTGTCTTCATTGGAGCTTTGGATAGATGAAATAAAATTGCAACCACT	ò a	CATGCAGACAGACAAAGATGTGGATAAAAGATGGAACTTCTTGTGGTTCAAATAAGGTT 186 
중 음	789 GGAGAAGCTAATGAGTTATTACACACATTTTTAAGAAGAAAAACATCTTATCTTGTTTTA 848 	& 8 	9 TGCAGGAATCAAAGATGTGAGTTCTTCATACTTGGGTTATGATTGTACTACTGACAAA 
දු පු	849 CGTCCTCATGATGTGGCATTTTACTTGTTTACAGAAAAGTCAAATTATGTTGGTGCA 908 	ò a	TGCAATGATAGAGGTGTATGCAATAACAAAAAGCACTGTCACTGTAGTGCTTCATTTA 198 [
රු සි	თ ო	& A	CCTCCAGATTGCTCAGTTCAATCAATCTATGGCCTGGTGGGAGTATTGACAGTGGCAAT 204 
රු සි	ACCATAAGTCTGGAATCACTTGCAGTTATTTTAGCTCAATTATTGAGCCTTAGTATGGGG	રું <del>વ</del>	TITCCACCIGIAGCIAIACCAGCCAGACICCCIGAAAGGCGCIACAIIGAGAACAIITAC 210
è 8	1029 ATCACTTATGATGACATTAACAAATGCCAGTGCTCAGGAGCTGTCTGCATTATGAATCCA 1088 	Ď.∵ó	09 CATTCCAAACCAATGAGATGACCATTTTTTTTTTTTTTT
ò	1089 GAAGCAATTCATTCAGTGGTGAAGATCTTTAGTAACTGCAGCTTCGAAGACTTTGCA 1148	λό da	2169 GTATTGCTATTATTGGTGAAAGTTAATTTCCAAAGSAAAAATGGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAAATGAAAAACTGAAAAAAAA

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72 ATGTGG---GTCTTGTTCTGCTCAGCGGGCTCGGCGGGCTGCGGATGGACAGTAATTTT 128
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DR Pfam; PF00200; Disintegrin; 1.

DR Pfam; PF00200; Disintegrin; 1.

DR PRINTS; PR00289; DISINTEGRIN.

DR PRINTS; PR00289; DISINTEGRIN.

DR PROSTIT; SM00606; ACR; 1.

SMART; SM00606; ACR; 1.

DR PROSTIT; PS00215; ADAM MEPRO; 1.

DR PROSTIT; PS00214; DISINTEGRIN 1; 1.

DR PROSTIT; PS00212; DISINTEGRIN 1; 1.

PROSTIT; PS00025; EGF 1; FALSE_NEG.

DR PROSTIT; PS01186; EGF 2; PALSE_NEG.

DR PROSTIT; PALSE_NEG.

DR PROSTIT; PS01186; EGF 2; PALSE_NEG.

DR PROSTIT; PALSE_NEG.

DR PROST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IleGluSerGlnValSerTyrLyg1leVallleGluGlyLysProTyrThrAlaAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 ATGCAAAAAACTTTTTACCCCATAATTTTAGAGTTTACAGTTATAGAGTGGCACAGGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular (Potential) Potential.
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MEDLINE=96341733; PubMed=8720115;

MEDLINE=96341733; PubMed=8720115;

MEDLINE=96341733; PubMed=8720115;

MOICHIGH evaluation of fertilin as an immunocontraceptive antigen and molecular cloning of the cynomolgus monkey fertilin beta subunit.";

MOICHIGH EAPLOAD Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during cfertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By eliminarity).
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SUBURILIT: Heterodimer with ADAMI/fertilin alpha.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed specifically in testis.
DOMAIN: A tripeptide motif (FDE) within disintegrin-like domain could mediate sperim-degg binding (By similarity).
Fould mediate sperim-megg binding (By similarity).
The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
SIMILARITY: Contains I disintegrin domain.
SIMILARITY: Contains I EGF-like domain.
                                                                                                                                                                                                                                                D AD02 MACFA STANDARD, PRT; 735 AA.

C 28478; C28472;
C 28478; C28472;
C 28478; C28472;
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 44, Last annotation update)
T 05-JUL-2004 (Rel. 44, Last annotation update)
T (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
Name-ADAM2; Synonyms-FTNB;
N Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
C Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
N NCBL TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Testis;
MEDLINE-95260313; PubMed=7741716;
Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
"Cloning and analysis of monkey fertilin reveals novel alpha subunit
                                 MESOPS, M12.950; --
INTERFOR, IRRO06586; ADAM cysteine.
InterFor, IRR006586; ADAM cysteine.
InterFor, IRR000742; EGF 2.
InterPro; IRR006209; EGF 11ke.
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DAGATE 2001 (Lichard).

BARAZ protein.

Si Homo sapiens (Human).

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa, Chordata; Catarrhini; Hominidae; Homo.

NOEL_TaxID=9606;

NOEL
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lux., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
REMBL; BC064547; AAH64547.1;
RINEEPRO; IPR001565; DAME Cysteine.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001509; Peptidase_M12B.
InterPro; IPR002809; Peptidase_M12B.
R Pfam; PF012009; Disintegrin; 1.
R Pfam; PF01421; ReprolyBlin; 1.
R Pfam; PF01421; ReprolyBlin; 1.
R Pfam; PF01421; ReprolyBlin; 1.
R PRNST; SM000664; Disintegrin; 1.
R SMART; SM000608; ACR; 1.
R SMART; SM000608; ACR; 1.
R PROSITE; PS50215; ADAM MEPRO; 1.
R PROSITE; PS50215; ADAM MEPRO; 1.
R PROSITE; PS50214; DISINTEGRIN 1; 1.
R PROSITE; PS50214; DISINTEGRIN 2; 1.
SEQUENCE 579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;
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Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;
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Matches:
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Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                    HisAlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysVal
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pfam; PF01562; Pep_M12B_propep; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOM: PD000664; Disintegrin; 1.
SWART; SW00608; ACR; 1.
SWART; SW00160; DISIN; 1.
SWART; SW00181; BGF; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS50216; EGF 3; 1.
SEQUENCE 735 AA; 81804 MW; 16F5554690AEF4AE CRC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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              AGAGGTGTATGCAATAACAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCAGAT 1997
                                                                                                             2058 GTAGCTATACCA---GCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCATTCC 2114
                                                                          GlnGlyValCygAganAsnLygArgAsnCygHisCygLygProThrTyrLeuProProAsn 642
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SUBGELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed specifically in testis.
TISSUE SPECIFICITY: Expressed specifically in testis.
DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain could mediate sperim/egg binding to egg integrin receptor and thus prim: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
SIMILARITY: Contains 1 disintegrin domain.
SIMILARITY: Contains 1 EGF-like domain.
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Biol. Reprod. 56:1245-1254(1997).
Biol. Reprod. 56:1245-1254(1997).
Pulorizous. Sperm surface membrane protein that may be involved in aperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm form the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its dishitegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
                                                                                                                           TGCTCAGTTCAATCAGATCTATGGCCTGGTGGGAGTATTGACAGTGGCAATTTTCCACCT
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"Biochemical and molecular characterization of bovine fertilin alpha
and beta (ADAM 1 and ADAM 2): a candidate sperm-egg binding/fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annocation update)
ADAM 2 precursor (A disintegrin and metalloproceinase domain (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
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MEDLINE=97304362; PubMed=9160725;
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SWART; SM00060; ACR; 1.

SWART; SM00181; BGF; 1.

PROSITE; PS00121; BJN MERRO; 1.

PROSITE; PS00122; BGF 1; PALSE_NEG.

PROSITE; PS00126; BGF 1; PALSE_NEG.

PROSITE; PS00186; BGF 2; PALSE_NEG.

CG11 adhesion; EGF-1iKe domain; Glycoprotein; Signal; Transmembrane.
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Conservative:
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                                                                                                                             InterPro; IPR006586; ADAM_cysteine.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001742; EGF 2.
InterPro; IPR006210; EGF 1.
InterPro; IPR006210; IEGF.
InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR001890; Peptidase_M12B.
InterPro; IPR001890; Peptidase_M12B.
InterPro; IPR001890; Peptidase_M12B.
Pfam; PF001562; Pep M12B_propep; 1.
Pfam; PF01421; Reprolygin; 1.
                         or send an email to license@isb-sib.ch).
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R InterPro; IPR006586; ADAM_Cysteine.
R InterPro; IPR001762; Disintegrin.
R InterPro; IPR000742; BGF2].
R InterPro; IPR000742; BGF2].
R InterPro; IPR000209; EGF7].
R InterPro; IPR002099; BGF7].
R Fam; PF01421; Reprolysin; 1.
R Pfam; Pf01421; Reprolysin; 1.
R Pfo1421; Pf01421; Pf01422; Ff152 MGC;
R Pf01421; Pf01421; Pf01422; Ff152 MGC;
R Pf01421; Pf01422; Ff152 MGC;
R Pf01421; Pf01422; Ff15423 MGC;
R Pf01421; Pf01422; Ff15423 MGC;
R Pf01422; Ff15423 MGC;
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed specifically in testis.
TISSUE SPECIFICITY: Expressed specifically in testis.
DOMAIN: A tripeptide motif (VGB) within disintegrin-like domain could mediate sperim-degg binding (By similarity).
First The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
SIMILARITY: Contains I disintegrin domain.
SIMILARITY: Contains I EGF-like domain.
                                                                                                                                                                                                                                  MEDLINE=97071141; PubMed=8914066;
Hardy C.M., Holland M.K.;
Hardy C.M., Holland M.K.;
Hordining and expression of recombinant rabbit fertilin.";
Mol. Reprod. Dev. 45:107-116(1996).

-I FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
28-FEB-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
(Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
Name-ADAM2; Synonyms-FTNB;
Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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18
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
DB:
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602

1934

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GTGAAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTATTCAAGCGATGAGCAA 2246
ATTTATGCCAACATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGTGATCATGCA 1814
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603 AsplysAlaCysValGluThrThrTyrValAsnLeuGlyCysThrLeuGlnAsnCysAsn
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AspAlaAlaLy8MetTrpValProAsnGlyAlaValCy8GlySerAsnLysIleCy8Arg
                                                                                                                663 GlyGlyGlyValProGlyIleGlyGlyLeuThrSerValGlyThrProProPheilePro
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                                                                   AATCAAAGATGTGTGTTCTTCATACTTGGGTTATGATTGTACTACTGACAAATGCAAT
                                                                                                      GATAGAGGTGTATGCAATAACAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCA
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|LeuCysProAspAspIleValIleGlnAsnGlyHisProCysGlyGluAsnGlnTrpIle
                                                                                                               GATGTGGCATTTTTACTTGTTTACAGAGAAAAGTCAAATTATGTTGGTGCAACCTTTCAA
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RELIAUGHINE-Sprague-Dawley; TISSUE=Testis;

MEDLINE-98019039; PubMed=9358007;

MEDLINE-98019039; PubMed=9358007;

MEDLINE-98019039; PubMed=9358007;

MEDLINE-98019039; Prayne J., Barker H.L., Jury J.A., Jones R.,

Rord W.C.L., Hall L.;

Toloning and sequence analysis of rat fertilin alpha and beta 
"Cloning and sequence analysis of rat fertilin alpha and beta 
"Cloning and sequence analysis of rat fertilin alpha and beta 
"Cloning and sequence analysis of rat fertilin alpha and beta 
"Cloning and sequence membrane protein that may be involved in

"Sperm-egg plaema membrane adhesion and fusion during

"Fertilization. Could have a direct role in sperm-zona binding or

migration of sperm from the uterus into the oviduct. Interactions

"It has a momentally to one or more integrins receptors on the

"Gainitegrin-like domain to one or more integrins receptors on the

"Similarity). Name-Adamā; Synonyme=Ftnb;
Rattus norvegicus (Rat).
Bukaryota; Metažoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI\_TaxID=10116; ŝ domain 063202; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) ADAM 2 precursor (A disintegrin and metalloproteinase (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).

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Query Match:
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DOMAIN: A tripeptide motif (NQE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).

PTM: The prodomain and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
(Potential)
(Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential). Metalloprotease-like.
                                                               similarity).
SIMILARITY: Belongs to peptidase family M12B.
SIMILARITY: Contains 1 disintegrin domain.
SIMILARITY: Contains 1 EGF-like domain.
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Cys-rich.
EGF-like.
By similarity.
By similarity.
Potential.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GloNac.)
                                                                                                                                                                                                                                                                    InterPro; IPR006886; ADAM cysteine.
InterPro; IPR00762; Disintegrin.
InterPro; IPR007762; Disintegrin.
InterPro; IPR006742; EGF_1.
InterPro; IPR006209; EGF_1.
InterPro; IPR008944; Nucleic_acid_OB.
InterPro; IPR008944; Nucleic_acid_OB.
InterPro; IPR002809; Peptidase_M12B.
InterPro; IPR002809; Peptidase_M12B.N.
Pfam; PF0050209; Disintegrin; 1.
ProDom; PD000664; Disintegrin; 1.
SWART; SW00608; ACR; 1.
SWART; SW00608; ACR; 1.
                                                                                                                                                                                                                       EMBL; X99794; CAA68127.1; ALT_INIT.
HSSP; P18619; 1FVL.
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RGD; 69299; Adam2.
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737 442 116 170

Length:
Matches:
Conservative:
Mismatches:

6.7e-179 2479.50 75.30% 59.65%

Percent Similarity: Best Local Similarity:

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2208 AAAAATGGAGAACTGAGGACTATTCAAGCGATGAGCAACCTGAAAGTGAGGGAACCT 2267
                                                                                                   SEQUENCE FROM N.A.

MEDINIB—2354681; PubMed=12466851; DOI=10.1038/nature01266;

N. Kadaki Y., Furunco M., Kabukawa T., Adachi J., Bono H., Koyosawa H.,

N. Kadaki Y., Furunco M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

N. Kadaki Y., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Guackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Guackenbush J.,

A Baldarelli R., Marsaich N., Marsuda H., Eatalov S., Beisel K.W.,

Baldarelli S., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,

Cassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Kanai A., Kawaji H., Kawasawa Y., Kodzierski R.M., King B.L.,

Randolt D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Savasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Savasi T., Reed J.C., Ranglasawa M., Shimada K.,

Namardo R., Wanner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Willming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Savolan M., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayaten N.,

Shiraki T., Waki K., Kawai J., Alawawa T., Pukuda S.,

Hira A., Hashizume W., Imotani K., Ishinagawa R.,

Namishino M., Sakai K., Sasaki D., Shibata K., Shinagawa H.,

Namishino M., Sanasi K., Sasaki D., Shibata K., Shinagawa H.,

Namaraki A., Sakai K., Sasaki D., Shibata K., Shinagawa H.,

Namaraki A., Sakai K., Sasaki D., Shibata K., Shinagawa H.,

Namaraki A., Sakai K.,
Birney B., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96019260; PubMed=7593287;
Evans J.P., Schultz R.M., Kopf G.S.;
EWOUSE sperm-egg plasma membrane interactions: analysis of role
egg integrins and the mouse sperm homologue of PH-30 (fertilin)
                                                                                                                                                                                                                                                                                                             ADO2_MOUSE STANDARD,

QGO71E, QG6814; Q95431, Q99QWJ0;

Q8-TEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

O5-WUL-2004 (Rel. 44, Last amoncation update)

O5-WUL-2004 (Rel. 44, Last amoncation update)

O5-WUL-2004 (Rel. 44, Last amoncation update)

(Fettilin beta subunit) (PH-30) (PH30) (PH30-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Gupta S.K., Palladino L.O., Mark G.E., Hollis Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell Sci. 108:3267-3278(1995).
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Mus musculus (Mouse).
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Nature 420:563-573(2002)
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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REMBL; REMOSSO; DISINTEGRIN.

REMART; SMO05064; DISINTEGRIN.

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REMART; SMO05064; DISINTEGRIN.

REMART; RESCO118; REPERPO; I.

REMART; RESCO118; REPERPO; I.

REMART; RESCO126; REF_1; FALSE_NEG.

REMART; REMOSSO; REF_1; FALSE_NEG.

REMOSTIE; PSSO1186; REF_2; FALSE_NEG.

REMOSTIE; PSSO1186; REF_2; FALSE_NEG.

REMOSTIE; PSSO126; REF_1; FALSE_NEG.

REMOSTIE; RE
            MEDLINE=95269891; PubMed=7750654; Wolfsberg T.G., Straight P.D., Gerena R.L., Huovila A.-P., Primakoff P., Myles D.G., White J.M.; Primakoff P., Myles D.G., White J.M.; PabMM, a widely distributed and developmentally regulated gene family encoding membrane proteins with a disintegrin and metalloprotease
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ProArgLeuGlnProSerTyrLy8---MetAlaValCy8GlyAsnGlyGluValGluGlu 399
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GluLysAspIleAspLeuArgAspSerGlnTyrLysIleArgSerIleLysProGlnArg 180
                                                                                                                ATTITIGITICATITIAATATIATIACAATIATICIGICTICATIGGAGCTITIGGATAAA
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|IlePheAlaProPheAsnLeuThrValIleLeuSerSerLeuGluPheTrpMetAspGlu
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SerCysLysLeuLysArgLysGlyGluValCysArgLeuAlaGlnAspGluCysAspVal
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                                GGGTCTGATACAACTGTTGTCGCTCAAAAGTTTTCCAGTTGATTGGATTGACGAATGCT
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PheTyrValValIleLeuValLeuIleGlyMetLeuValLys0ValTyrSerGlnArgMet 714
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||||:::::
|LeuLysLeuArgSerAlaThrVallleTyrAlaAsn1leSerGlyHisValCysValSer
                                                                                                                   TTACAAATTCCAAGAGCCACTATTATTATGCCAACATAAGTGGACATCTCTGCATTGCT
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LeuGluTyrProGlnGlyHisAsnGluSerGlnLysMetTrpValArgAspGlyThrVal
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| AspCysAsnLeuGluLysCysAsnHisHisGlyValCysAsnAsnLysLysAsnCysHis
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MEDLINE=94068486; PubMed=8248170;
Wolfsberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi
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Blobel C.P., Wolfsberg T.G., Turck C.W., Myles D.G., Primakoff
White J.M.;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2 (Fertilin beta subunit) (PH-30) (PH30).
Name-ADAM2; Synonyms=FTNB;
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
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Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                                                                                                                             192
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its moch ono-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain; Glycoprotein; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular (Potential) Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential)
Metalloprotease-like.
Disintegrin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyg-rich.
EGF-like.
By similarity.
By similarity.
Potential.
By similarity.
By similarity.
By similarity.
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR006210; EGF 2.
InterPro; IPR006210; EGF 2.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR00289; Disintegrin; 1.
PRINTS; PR00289; DISINTEGRIN; 1.
SMART; SM000684; Disintegrin; 1.
SMART; SM000608; ACR; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS56215; ADAM MEPRO; 1.
PROSITE; PS60217; DISINTEGRIN 1; 1.
PROSITE; PS56214; DISINTEGRIN 2; 1.
PROSITE; PS60214; DGF 1; FALSE NEG.
PROSITE; PS60186; EGF 2; FALSE NEG.
PROSITE; PS56026; EGF 3; 1.
Cell adhesion; EGF-1ike domain; Glyco.
          -1- FUNCTION: Sperm surface membrane
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Nature 356:248-252(1992)
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735 AA;
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DISULFID
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ATAAGTCTGGAATCACTTGCAGTTATTTAGCTCAATTATTGAGCCTTAGTATGGGGATC 1031
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163 ABRUVAIVAITYLYBISILELYBSEXILIELYBSEXSEXVAIARG---ThrHisTyrIleGlu 181
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 735
413
125
182
16
Length:
Matches:
Conservative:
Mismatches:
Indels:
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2.76e-167
2326.00
73.10%
56.11%
48.50%
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                                              GCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAACTGCAGCTTCGAAGACTTTGCACAT 1151
                                                                                                                                                                                       ACTGAACAGGATTGTGCCCTTATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTT 1331
                                                                                                                                                                                                                                    AAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGCGAAAACTGTCTATTTATGTCAAAA 1391
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ProProAsnCysGluThrGlnAspSerThrLysProGlyGlySerValAspSerGlyAsn 658
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|-----ProGluThrTyrPheValGluGly 672
           :::
ArgSerAsnProValCysGlyAsnAsnArgValGluGlnGlyGluAspCysAspCysGly 401
                                                         TITATITICAAAGCAGAAGTCCCAGTGTCTTCACAATCAGCCTCGCTTAGATCCTTTTTTC
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LeuArgTyrGluProIle------
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                                                                                                                         2222
2162
                                                                                                                                                          Frayne J., Jury J.A., Barker H.L., Perry A.C.F., Jones R., Hall L.;
"Macaque MDC family of proteins: sequence analysis, tissue
distribution and processing in the male reproductive tract.";
Mol. Hum. Reprod. 4:429-437 (1998).

-1- FUNCTION: Sperm surface membrane protein that may be involved in
spermatogenesis and fertilization. This is a non catalytic
metalloprocease-like protein (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUE SPECTICITY: Expressed predominantly in adult and
prepubertal testis.

-1- DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain
could be involved in the binding (By similarity).

-1- PTM: The prodomain and the metalloprotease-like domain are cleaved
during the epididymal maturation of the spermatozoa.

-1- SIMILARITY: Contains I EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
20-7-7-2004 (Rel. 45, Last annotation update)
01-07-2004 (Rel. 45, Last annotation update)
ADAM 18 precursor (A disintegrin and metalloproteinase domain 18)
(Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-
rich protein III) (tMDC III).
Name-ADAM18; Synonyms-TMDC3;
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordats; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                          673 AlaTyTHisThrLysSerArgLysTrpProPhePheLeulleIleProPhePheVallle
                                                                                                                     TICTGTGTACTGATTGCTATAATGGTGAAAGTTAATTTCCAAAGGAAAAAATGGAGAACT
GAGGACTATTCAAGCGATGAGCAACCTGAAAGTGAGAGTGAACCTAAA
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Interpro; 1PR001590; Peptidase M12B.
Interpro; 1PR002870; Peptidase_M12B_N.
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InterPro; IPR001762; Disintegrin.
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Pfam; PF01562; Pep_M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
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NCBI_TaxID=9541;
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SMART; SM00608; ACR; 1
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PheLeuLeuAlaLeuLeuThrGluLeuGlyArgLeuGlnAlaHisValGlySerGluGly 22

      SMART; SM00050; DISIN; 1.

      PROSITE; PS50215; ADAM MEPRO; 1.

      PROSITE; PS0427; DISINTEGRIN 1; FALSE_NEG.

      PROSITE; PS00022; EGF 1; FALSE_NEG.

      PROSITE; PS010186; EGF 2; PALSE_NEG.

      PROSITE; PS50026; EGF 1; FALSE_NEG.

      PROSITE; PS50026; EGF 3; 1.

      EGF-like domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.

      SIGNAL
      1

      PROSITE; PS00025; EGF 3; 1.
      PROSITE; PS00025; EGF 3; 1.

      EGF-like domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.
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      PROSITE; PROSITE; PS00025; EGF 3; 1.
      ADAM 18.

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                                                                                                                                                                                                                                                                        Potential.

Yetoplasmic (Potential).

Metalloprocease-like.

Disintegrin-like.

SGF-like.

BGF-like.

BGF-like.

BG similarity.

Potential.

By similarity.

By similarity.

By similarity.

Nolinked (GlCNAC...) (PN.

Nolinked (GlCNAC...) 
                                                                                                                                                                                                                                                        Extracellular (Potential)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
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TRANSMEM
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DISULFID
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421 AsnThrCysLysLeuLysGlySerValLysCysGlySerGlyProCysCysThrSerLys 440
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143 MetLysasnasnaspProasnValSerIleLeualaGluasnTyrSerHisIleTrpGln 162
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GTAAAACATAAGAAAGCAGATGTTTCCTTATAT-----AATGAGAAGGATATTGAATCA
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ValAsnSerLeuHisGluThrSerGluAsnCysGlyPheLysAsnSerGlnProLeuPro 540
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28-FEB-2003 (Rel. 41, Last sequence update)
01-6CT-2004 (Rel. 45, Last annotation update)
ADAM 18 precursor (A disintegrin and metalloproteinase domain 18)
(Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-
rich protein III) (+MDC III)
Name=ADAM18; Synonyms-TWDC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGAAGCTGACAATCTGCAGTGCGGAAAATTAATATGTAAATATGTAGGTAAATTTTTA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@isb-sib.ch).
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SUBCELLULAR LOCATION: Type I membrane protein.

TISSUB SPECIFICITY: Expressed specifically in testis.

DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).

PTM: The prodomain and the metalloprotease-like domain are cleaved during the epididymal maturation of the spermatozoa (By
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Metalloprotease-like.
Disintegrin-like.
                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: Belongs to peptidase family M12B.
-i- SIMILARITY: Contains 1 disintegrin domain.
-i- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS, M12.957; -... Genew; HGNC:196; ADANIB. Genew; HGNC:196; ADANIB. GO; GO:0005624; C.membrane fraction; TAS. GO; 0006237; F.metallopeptidase activity; TAS. GO; GO:0007283; P:spermatogenesis; TAS.
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GAGTATTGACAGTGGCAATTTTCCACCTGTAGCTATACCAGCCACACTC 2078 ACTTATGATGACATTAACAAATGCCAGGGCTCAGGAGCTGTCTGCATT 1079 TOGATCATCTGCATCATCCCCAGAAAACCACTATGTTCAGACTGGGCAT 1493 CYGTAGTGCTTCATATTTACCTCCAGATTGCTCAGTTCAATCAGATCTA 2018 GCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAACTGCAGCTTCGAA 1139 TTTATTTCAAAGCAGAAGTCCCAGTGTCTTCACAATCAGCCTCGCTTA 1199 AAACAGCAAAGCAGTGTGGTAATGCAAAGCTGGAAGCAGGAGGAG 1259 ACTGAACAGGATTGTGCCCTTATTGGAGAAACATGCTGTGATATTGCC 1319 AAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGC---GAAAACTGT 1376 AAAGAAAGAATGTGTAGGCCTTCCTTTGAA---GAATGCGACCTCCCT 1433 SAATCAATGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAA 1553 ATTTGGCAAAGAAGTAGAGTTTGGCCCTTCAGAATGTTATTCTCACCTT 1613 RGATGTATCTGGAAACTGTGGTATAAGTGATTCAGGATACACACAGTGT 1673 | ICTGCAGTGCGGAAATTAATATGTAAATATGTAGGTAAATTTTTATTA 1733 GAATTTGCCAGTGATCATGCAGACAGCCAAAAGATGTGGGATAAAAGAT 1841 rggitcaaataaggitigcaggaatcaaagargigtgaggttcttcatac 1901 501 ||||||| rSerMetArgSerAspGlyThrAspAsn----AlaTyrValAlaAsp 599 |||| 3GlyProGluMetTyrCysValAsnLysThrCysArgLysValHisLeu 619 IleGlyLeuGluGlyPheSerValIleIleAlaGlnLeuLeuGlyLeu 323 

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Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chow C., Crowley C., Currell B., Deuel B., Dowd Eaton D., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagtes A. Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Ysnsura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., "McCoowski P.,"
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PROSITE, PS60215, ADAM MERPO, 1.
PROSITE, PS50214, DISINTEGRIN 2, 1.
PROSITE, PS500216, EGF_2; UNKNÖMN_1.
PROSITE, PS50026, EGF_3; 1.
Integrin, Metalloprotease, Protease
SEQUENCE 787 AA, 87933 MW; 3D84CA
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Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
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MALSTANDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Indeptins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchento L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Marting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Marra M.A., Jones S.J., Marra M.A., Schalba D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Shalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Shein J.E., Schnerch A., Schein J.E., Schnerch A., Shein J.E., Schnerch A., Schein J.E., 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
A disintegrin and metalloprotease domain 32 (Similar to MDC
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MEDLINE=22887296; PubMed=12975309;
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Dowd P.
                                                                                                                                                                                                                                                                                  effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment. ^{n}_{j} Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                    "The secreted protein discovery initiative (SPDI), a large-scale
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558 ThrArgLysProPheHisGlnGluAsnGlyAspVallleTyrAlaPheValArgAspSer
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|LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys
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SEQUENCE FROM N.A.
PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin
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Mammalia; Butheria; Primata; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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"The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D. Yis, S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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Genome Res. 13:2265-2270(2003).
EMBL; AY358739; AAQ89099.1; -.
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PROSITE; PSS0214; DISINTEGRIN 2; 1.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
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Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausper R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McWam P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
                                                                                                         1899 TACTTG-----GGTTATGATTGTACTACTGACAAATGCAATGATAGAGGTGTATGC 1949
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1950 AATAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCAGATTGCTCAGA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
disintegrin and metalloprotease domain 32.
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MEROPS; MIJ.960; ...

R GO; GO:0004222; F:metalloendopeptidase activity; IEA.

GO; GO:0004229; F:mtegrin-mediated signaling pathway; IEA.

GO; GO:0007229; P:proteolysis and peptidolysis; IEA.

R InterPro; IPRO0586; ADAM cysteine.

R InterPro; IPRO0586; ADAM cysteine.

R InterPro; IPRO06049; EGF 1; EGF 1; EGF 2.

R InterPro; IPRO0509; EGF 1; EGF 1; EGF 2.

R InterPro; IPRO0509; EGF 1; EGF 1; EGF 2.

R InterPro; IPRO0509; Peptidase MI2B.

R Ffam; PF00200; Disintegrin; 1.

R SWART; SW00608; ADS; 1.

R SWART; SW00608; ADS; 1.
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                                                                                                                                                 GGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTTGGCCCTTCAGAATGT 1601
                                                                                281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCys1leThrArgTyrSer 300
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TyrTrpGlySerAspSerMetlleValThrAsnLysVallleGlulleValGlyLeuAla 220
                                                                        AATGCTATTTTTGTTTCATTTAATATTACAATTATTCTGTCTTCATTGGAGCTTTGGATA 764
                                                                                                                                                                                        GAAAAGTCAAATTATGTTGGTGCAACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCA 944
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                                                                                                             GATGAAAATAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACACACATTTTTAAGA 824
          ProAspLeuPheProLeuTyrLeuGluMetHislleValValAspLysThrLeuTyrAsp
                                    CATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTCCAGTTGATTGGATTGACG
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                                                                                                                                                                                                                                                               TACTTG-------GGTTATGATTGTACTACTGACAAATGCAATGATAGAGGTGTATGC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
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US-09-813-819-4
US-09-920-048-4
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Command line parameters:
-MODELE frame+ n2p.model - DEV=Xlp
-MODELE frame+ n2p.model - DEV=Xlp
-G-Cgn2_1/USF7O_spool_p/US10054683/runat_10012005_174511_15520/app_query.fasta_1.2823
-G-Cgn2_1/USF7O_spool_p/US10054683/runat_10012005_174511_15520/app_query.fasta_1.2823
-DEJESDE Patents AA -QFWT=fastan - SUFFTX=n2p.rai - MINNATCH=0.1 - LOOPCL=0
-LIGN=20 - UNITS=Dits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=buman40.cdi
-LIST=6 - DOCALIGN=200 - THE SCORE=por - THR MAX=100 - THR MINED - ALICEN=15
-MODE=LOCAL - OUTFWT=pto - NORM=ext - HEAPS/IZE=500 - MINLEN=0 - MAXICEN=200000000
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-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS:1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 70, Appli
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11. /Ggn2_6/ptodatca/1/iaa/5A_COMB.pep:*
12. /Ggn2_6/ptodatca/1/iaa/5B_COMB.pep:*
31. /Ggn2_6/ptodatca/1/iaa/6A_COMB.pep:*
41. /Ggn2_6/ptodatca/1/iaa/6B_COMB.pep:*
42. /Ggn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*
43. /Ggn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*
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47. /Ggn2_6/ptodatca/1/iaa/backfiles1.pep:*
48. /Ggn2_6/ptodatca/1/iaa/backfiles1.pep:*
49. /Ggn2
                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                    protein search, using frame_plus_n2p model
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PCT-USS5-07295-8
US-08-264-101-2
US-08-765-243-2
US-08-765-243-6
PCT-US95-07295-6
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US-08-765-243-4
US-10-000-489-70
US-10-140-002-116
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Listing first 45 summaries
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Jatabase

Result Š

281 PheGlnGlyLysMetCysAspAlaAsnTyrAlaGlyGlyValValLeuHisProArgThr 300 972 ATAAGTCTGGAATCACTTGCAGTTATTTTAGCTCAATTATTGAGCCTTAGTAGTGGGATC 1031	15.2	
	\$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8	ф 
TYPE: amino acid   TYPE: mino acid   TYPE: protein   TYPE: p	132 AGCTGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Oy 912 TTTCAAGGAAGATGTGTATGCAACTATGCAGGAGGTGTTGTTCTGCACCCCAGAACC 971

us-10-054-683-18.n2p.rai

Db 21 SerLeuProValGlnIleThrValProGlutysIleArgSerIleIleLysGluGlyIle 40	2171  Qy 252 CAAAAAACTTTTTACCCCATAATTTAGGGTTTACAGTTATGGGCACAGGAATTATG 700  Db 61 GlaLvaRanPheLeuProHisAanPheArqValTyrSerTyrSerGlyThrGlyIeMet	2231  Qy 312 AAACCACTTGACCAAGATTTTCAGAATTTCTGCCACTACCAGGGTATATTGAAGGTTAT  720  B	372	432 AATGTTAGTTATGGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAACATGTAATTTAC	Oy 492 CAAGTAAAACATAAGAAAGCAGATGTTTCCTTATATAATGAGAAGGATATTGAATCAAGA 5	Qy         552 GATCTGTCCTTTAAATTACAAAGCGCAGGCAGGAAGATTTTGCAAAGTATATAGAA         611	Oy 612 ATGCATGTTATAGTTGAAAAACAATTGTATAATCATATGGGGTCTGATACAACTGTTGTC 671	Oy 672 GCTCAAAAGTTTTCCAGTTGATTGAATGCTATTTTTTTTT	Oy 732 ACAATTATTCTGTCTTTGGAGCTTTGGATAGATGAAAATAAAATTGCAACCACTGGA 791	Oy 792 GAAGCTAATGAGTTATTACACACATTTTTAAGATGGAAAACATCTTATCTTGTTTTACGT 851	Qy         85.2 CCTCATGATGTGGCATTTTTACTTGTTTACAGAAAAGTCAAATTATGTTGGTGCAACC         91.1           Db         26.1 ProHisAspValAlaPheLeuLeuValTyzArgGluLysSerAsnTyrValGlyAlaThr         280	Oy 912 TTTCAAGGAAGATGTGTGATGCAAACTATGCAGGAGGTGTTGTTCTGCACCCCAGAACC 971	Oy 972 ATAAGTCTGGAATCACTTGCAGTTATTTTAGCTCAATTATTGAGCCTTAGTATGGGGATC 1	1032	Oy 1092 GCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAACTGCAGCTTCGAAGACTTTGCACAT 11	131 Qy 1152	20 20 20 20 20 2122 AAACAGCAAGCAGCAGTGTGTGTAATGCAAAGCTGGAAGGAGGAGGAGTGACTGTGGG 2111
2052 CCACCTGTAGCTATACCAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCAI 	2112 TCCAAACCAATGAGATGGCCATTTTTCTTATTCATTCCTTTTTTTT	2172 CTGATTGCTATAATGGTGAAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 	2232 TCAAGCGATGAGCAACCTGAAAGTGAGTGAACCTAAAGGG 2273 	licati ATION:	APPLICANT: ALVES, KUNDETH APPLICANT: GUPTA, SUNIL K. APPLICANT: HOLLIS, GREGORY F. TITLE OF INVENTION: CONTRACEPTIVE VACCINE	NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESSS: ADDRESSEE: MARY A. APPOLLINA STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE	CITY: RAHWAY STATE: NJ COUNTRY: USA ZIP: 07065	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIDLE OPERATING SYSTEM: PC-DOS/MS-DOS	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/07295 FILING DATE:	CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: APPOLLINA, MARY A REGISTRATION NUMBER: 34,087	7 4 0 4 6	1236	IOPOLOGI: Illegi MOLECULE TYPE: protein CT-US95-07295-8	Alignment Scores:  Pred. No.:  Score:  Score:  100.00\$  Ministry:  100.00\$  Ministry:  M	100.00 intellactures: 83.07% Indels: 5 Gaps:	US-10-054-683-18 (1-2640) x PCT-US95-07295-8 (1-734) Qy 72 AIGIGGGTCTTGTTTTTGGGGGGTCGGGGGTGGGATGAAATTTTGA	

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COUNTRY: USAN
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,101
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 19244
TELEPHONE: (908) 594-4720
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENNYTH: 651 amino acids
                                                                      ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 B. LINCOLN AVENUE
CITY: RAHWAY
COUNTRY: USA
       APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: Bingle
TOPOLOGY: linear
GENERAL INFORMATION:
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                                                                                                                                        TCTGCATCATGCCCCAGAAAACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAATCAA 1511
                                                                                                                                                                                 TGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACATTTGGC 1571
                                                                                                                                                                                                                           AAAGAAGTAGAGTTTGGCCCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGATGTA 1631
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                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                  3551.00
100.00%
100.00%
74.04%
TYPE: protein
                                                                     Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                          Alignment Scores:
Pred. No.:
              US-08-264-101-2
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Sequence 2, Application US/08264101 Patent No. 5693496

US-08-264-101-2

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REFISHARTION NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEFAK: (908)594-3462
TELEFAK: (908)594-3462
TELEFAK: (508)594-3462
TELEFAK: (51 mino acids
TENGRATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 mino acids
TOPOLOGY: linear
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STRRET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
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; Patent No. 593578
; GENERAL INFORMATION:
; PAPLICANT: ALVES, KENNETH
APPLICANT: HOLLIS, GENCORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: MARY A. APPOLLINA
COUNTRY: B.O. BOX 2000, 126 E. LINCOLN AVENU
CITY: RAHWAY
STREET: NJ
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BACTATION DATA:
CURRENT APPLICATION NUMBER: US/08/765,243
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                                                                                                     CITY: RAHMAY
STATE: NJ
STATE: NJ
COUNTRY: USA
ZIP: 07055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION DATM:
APPLICATION NUMBER: PCT/US95/07295
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650
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Matches:
Conservative:
Mismatches:
Indels:
                          APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSE:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-054-683-18 (1-2640) x PCT-US95-07295-2 (1-651)
                                                                                                                                                                                                                                ATTORNEY AGENT INPORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INPORMATION:
TELEPRAN: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: almino acids
TYPE: TYPE: protein
          Sequence 2, Application PC/TUS9507295 GENERAL INFORMATION:
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100.00%
100.00%
74.04%
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Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Ouery Match:
5
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CLASSIFICATION:
PCT-US95-07295-2
                                                                                                                                                                                                                                                                                                                                                                 HOLECULE TYPE PCT-US95-2
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Qy 1764	AAC		TOPOLOGY: linear
Db 482			; MOLECULE TYPE: protein US-08-765-243-6
Oy 1824	AAGATGTGGATAAAAGATGGAACTTCTTGTGGTTCAAATAAGGTTTGCAGGAATCAAAGA 1883 		Alignment Scores: 7.98e-Pred. No.: 2440.0
П	TGTGTGAGTTCTTCAIACTTGGGTTATGATTGTACTGCTGACGAATGCAATGATGGAGGGGGTTTGTACTGGGGTTATGATGGGGGTTGTACTGGGGTATGTACTGGGGTTGTACTGGGGTATGTACTGGGGTATGTACTGGGGGGGG	· ·	Percent Similarity: 75.71% Best Local Similarity: 59.57% Query Match: 2
Qy 1944	GTA	-	US-10-054-683-18 (1-2640) x US
Db 542		*2	Qy 78 GTCTTGTTTCTGCTCA
Oy 2004	GTTCAATCAGATCTATGGCCTGGTGGGAGTATTGACAGTGGCAATTTTCCACTGTAGCT 2063 		Db 4 IleLeuLeuLeuLeuS
	vardinisernsbyneurityeroerystycertrensbyneurraynsmiseroeren		
Ly 2064 Db 582	ATACCAGCCAGACTCCCTGAAGGGGCTACATTGAGAACATTTGACCATTCCAAACCATG	F	DB 24 GIYIDIYANGGILLIYBL OY 180 AAGGAAGGAATTGAAT
Qy 2124	AGATGGCCATTTTTTCTTATTCATTCCTTTATTTTTTTTT		Db 44 SerAsnGlyTyrGluT
Db 602			Qy 240 GTGAATTTAATGCAAA
Qy 2184 Db 622	ATGGTGAAAGTTAATTTCCAAAGGAAAAATGGAGAACTGAGGACTATTCAAGGGATGAG 2243		Db 64 LeuaspieuMetGlni Qy 300 ACAGGAATTATGAAAC
Qy 2244			Db 84 AlaGlyIleMetArgS
Db 642	-G		Qy 360 ATTGAAGGTTATCCAA
RESULT 6 US-08-765-243-6	9-	-	Db 104 IleGluGlyTyrProA
; Sequence 6, ; Patent No.	Application US/08765243 5935578		QY 420 CTACAGTTTGAAAATG
GENERAL IN	FORMATION: T: ALVES, KENNETH		Db 124 LeuGlnPheGlyAsnV
, APPLICAN	, APPLICANT: GUPTA, SUNIL K. , APPLICANT: HOLLIS, GREGORY F.		Qy 480 CAIGTAATTTACCAAG
; TITLE OF	'INVENTION: CONTRACEPTIVE VACCINE OF SEQUENCES: 8		
; CORRESPO ; ADDRES.	NDENCE ADDRESS: SEE: MARY A. APPOLLINA		Oy 540 ATTGAATCAAGAGATC
; STREET	: P.O. BOX 2000, 126 E. LINCOLN AVENUE RAHWAY		
; STATE:	NJ IX: USA		Oy 600 AAGTATATAGAAATGC
; ZIP: ; COMPUTER	07065 READABLE FORM:		
; MEDIUM	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible		Oy 660 ACAACTGTTGTCGCTC
; OPERAT	'ING SYSTEM: PC-DOS/MS-DOS .RE: PatentIn Release #1.0, Version #1.30	-	
; CURRENT ; APPLIC	APPLICATION DATA: .ATION NUMBER: US/08/765,243	· <del></del> .	Oy 720 TCATTTAATATTACAA
; FILING	: DATE: FICATION: 536		Db 224 ProPheAsnLeuThrV
, ATTORNEY , NAME:	//agent information: appollina, mary a		Qy 780 GCAACCACTGGAGAAG
; REGIST ; REFERE	RATION NUMBER: 34,087 INCE/DOCKET NUMBER: 19244Y		Db 244 LeuThrThrGlyAspA
; TELECOMM	IUNICATION INFORMATION: IONE: (908)594-3462		QY 840 CTTGTTTTACGTCCTC
; TELEFAX;	X: (908)594-4720 IN FOR SEQ ID NO: 6:		Db 264 LeuValLeuArgProF
	SEQUENCE CHARACTERISTICS: LENGTH: 735 amino acids TYPE: amino acid		Qy 900 GTTGGTGCAACCTTTC            :::  Db 284 ValGlvAlaThrTvrG
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359
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                                                                                                                                               CATGATGTGGCATTTTTACTTGTTTACAGAGAAAAGTCAAATTAT
                                                                                       ACCACTIGACCAAGATTTTCAGAATTTCTGCCACTACCAAGGGTAT
735
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                             S-08-765-243-6 (1-735)
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2040 AGTGGCAATTTTCCACCTGTAGCTATACCAGCCAGACTCCCTGAAAGGCGCTACATTGAG 2099
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
FILING DATE:
PILING DATE:
ATPORNEY/AGENT INFORMATION:
ATPORNEY/AGENT INFORMATION:
ATPORTATION NUMBER: 34,087
REGISTRATION NUMBER: 34,087
REGISTRATION NUMBER: 34,087
TELEFRONCE/FOCKET NUMBER: 19244Y
TELEFRANCE/FOCKET NUMBER: 19244Y
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Matches:
Conservative:
Mismatches:
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STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALVES, KENNETH
APPLICANT: GUFTA, SUNIL K.
APPLICANT: HOLLIS, GRECORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application PC/TUS9507295
GENERAL INFORMATION:
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amino acid
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Best Local Similarity:
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1260 403 1320 422 1380 442	Oy 1440 TGCAATGGATCATCTGCA  162 CysAsnGlyThrSerGlu  QY 1500 GGACTGAATCAATGGATC  Db 481 ASpAsnArgLySTrp11e  Qy 1560 GACACATTTGGCAAAGAP  Db 501 AspLeuPheGly11eAsg	Oy 1620 AAGACTGATATCTGGB Db 521 LyBSerAsp11eSerGly Oy 1680 GACAATCTGCAGTGCGGP ::::: Db 541 A8nAspArgMetCAGTGTG OY 1740 CCAAGAGCCACTTATT Db 561 ARGSERAITHTTATTATTATTATTATTATTATTATTATTATTATTATT	1800 581 1860 601	1920 621 1980 641 2040	Oy 2100 AACATTTACCATTCCAAT  1:
180 AAGGAAGGAATGGAAGGCATCCTACAAATTGAAGGGAAACCATATACT 239	360 ATTGAAGGTTATCCAAAATCTGTGGTGATGCTAGCACATGTACTGGACTCAGGGGCGTA 419 104 IleGluGlyfyrProAsnSerMetValIleValSerThrCysThrGlyLeuArgGlyPhe 123 420 CTACAGTTTGAAAATGTTATGGAATAGAACCCTGGAGTCTTCAGTTGGCTTTGAA 479 124 LeuGlnPheGlyAsnValSerTyrGlyIleGluProLeuGluSerSerSerGlyPheGlu 143 480 CATGTAATTACCAAGTAAAACATAAGAAACCAGATTCCTTATATAATGAGAAGGAT 539 11	ATCAGGAGTCTGTCTTTAATTACAAGGGGAGAGCCACAGCAAGATTTGCA 59  THILLING STATEMENT ST	204 ThralarievalThrGlnLysliepheGlnLeuiledlyLeunlaAenAlariepheAla 223 720 TCATTTAATATTACAATTATCGTCTTCATTGGAGCTTTGGATAGAAAAAAATT 779 720 TCATTTAATATTATATTATCGTCTTCATTGGAGCTTTGGATAGAAAAAAATT 779 224 ProPheAsnLeuThrValIleLeuSerSerLeuGlubheTrpMetAepGluAenLyslle 243 780 GCAACCACTGGAGAGAGCTAATGAGTATTATACATGGAAAACATCTTAT 839 781 GCAACCACTGGAGAGAGAGATATTACACATTTTTAAGATGGAAAACATCTTAT 839 244 LeuThrThrGlyAepAlaAenLysLeuLeuTyrArgPheLeuLysfTpLysGlnSerTyr 263	_ ∞ ω ω 'H ω	ACTATGGGGATCACTTATGATGACAATGCCAGTGCTCAGGAGCTGTCTGCATT 1
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PheTyrValValIleLeuValLeuIleGlyMetLeuValLyaValTyrSerGlnArgMet 436
                        122 AspGluIleCysAspCysGly---LysLysGlyCysAlaGluMetProProProCysCys 140
                                                             GATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGCGAA
                                                                                                                                                                                                                          1431 CCTGAATATTGCAATGGATCATCTGCATCATGCCCAGAAAACCACTATGTTCAGACTGGG
                                                                                                                                                                                                                                             ; Sequence 4, Application US/08765243; Patent No. 5935578; GENERAL INFORMATION: APPLICANT: APPLICANT: GUPTA, SUNIL K.
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US-08-765-243-4
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|SerMetGluAgpPheSerLysPheIleThrSerGlnSerSerHisCysLeuGlnAsnGln 102
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265
74
1115
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                       ALUKESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-054-683-18 (1-2640) x US-08-264-101-4 (1-457)
APPLICANT: GUPTA, SUNIL K.

APPLICANT: HOLLIS, GREGORY F.

TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: MADV. S.

STEPPTION OF STE
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFTCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELEPHONE: (908) 594-4720
TELEPHONE: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908)594-4720
INPORMATION POS SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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1512.00
73.70%
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Best Local Similarity:
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Pred. No.:
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300 LeugluTyrProGlnGlyHi8AsnGluSerGlnLysWetTrpValArgAspGlyThrVal 319
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pheTyrValValIleLeuValLeuIleGlyMetLeuValLy8ValTyrSerGlnArgMet 436
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                                                               CCTGAATATTGCAATGGATCATCTGCATCATGCCCAGAAAACCACTATGTTCAGACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application PC/TUS9507295
GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUFTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
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ProThrLeuGlnProSerTyrLys---MetAlaValCysGlyAsnGlyGluValGluGlu 121
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CALL: 1,000

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Parentin Pelease #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,243

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: APPOLLINA, MARY A

REGISTRATION NUMBER: 34,087

REFERENCE/DOCKET NUMBER: 19244Y

TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457
265
74
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                            ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 B. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
STATE: NJ
ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-054-683-18 (1-2640) x US-08-765-243-4 (1-457)
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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1512.00
73.70%
57.61%
31.53%
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 457 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                              (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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PheTyrValValIleLeuValLeuIleGlyMetLeuValLy8ValTyrSerGlnArgMet 436
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161 SerCysLysLeuLysArgLysGlyGluValCysArgLeuAlaGlnAspGluCysAspVal
                                                                                                                                              CATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATGAGTGGGGGATAAA
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GlnCysGlnAspLeuPheGly11eAspAlaGlyPheGlySerSerGluCysPheTrpGlu
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                   1431 CCTGAATATTGCAATGGATCATCTGCATCATGCCCAGAAAACCACTATGTTCAGACTGGG
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Patent No. 6794363
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPRENCE: 91.US6.DIV
CURRENT APPLICATION HUMAN: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
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ProThrLeuGlnProSerTyrLy8---MetAlaValCysGlyAsnGlyGluValGluGlu 121
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| AspGluIleCysAspCysGly---LysLysGlyCysAlaGluMetProProProCysCys 140
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Matches:
Conservative:
Mismatches:
             ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
COUNTEY: USA
ZIP: 07065
                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
FILING DATE:
FLING DATE:
FLING DATE:
FLING DATE:
FLILO DATE:
FLILO DATE:
FLILO DATE:
FLILO DATE:
FLILO NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acide
TYPE:
COMPUTER TO A STORM TO A SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acide
TYPE:
COMPUTER TO A STORM TO A SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-054-683-18 (1-2640) x PCT-US95-07295-4 (1-457)
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Gaps:
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73.70%
57.61%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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| HisValLeuHisLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160
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LeuLygGluGInProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
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LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe
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307
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261
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: PCT/IBO1/01715

PRIOR PILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-06-16

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 112

SOFTWARE: UP ALCATION NUMBER: US 60/293,574

SOFTWARE: UP ALCATION NUMBER: UP ALCATION 
                                                                                                                                                                                                                                                                                                                                                                              1.4e-133
1506.50
58.62%
40.72%
31.41%
                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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; LOCATION: 1..16
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CACCCCAGAACCATAAGTCTGGAATCACTTGCAGTTATTTAGCTCAATTATTGAGCCTT 1019
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Mismatches:
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Godward, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Tummas, Daniel
APPLICANT: Watanabbe, Colin K
APPLICANT: Watanabbe, Colin K
APPLICANT: Watanabbe, Colin K
APPLICANT: Anany, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1G59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
                                                                                          1899 TACTIG------GGTTATGATTGTACTACTGACAAATGCAATGATAGAGGTGTATGC 1949
                                                                                                                                                                                                          1950 AATAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCAGATTGCTCAGTTCAA 2009
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                                                 CTCTGCATTGCTGTGGAATTTTGCCAGTGATCATGCAGACAGCCAAAAGATGTGGATAAAA
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Patent No. 6725730
GENERAL INFORMATION:
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Filvaroff, Ellen
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CORGANISM: Homo Sapien
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••	::: LysSerAspAlaClnSerThrValTyrSerTyrIleClnAspHisValCysValSerIleGAATTTGCCAGTGATCATGCCAGACGACAAAGATGTGGATAAAAGAT AlaThrGlySerSerMetArgSerAspGlyThrAspAsnAlaTyrValAlaAsp
; SEQ ID NO 204 ; LENGTH; 790 ; TYPE: PRT ; ORGANISM: Homo Sapien US-10-140-002-204	ATATGTAAATATGT     AlaCysvalGlnPr AACATAAGTGGACA
CURRENT APPLICATION NUMBER: US/10; CURRENT FILING DATE: 2002-05-06; Prior Application removed - See P; NUMBER OF SEQ ID NOS: 550	
HPPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TITLE OF INVENTION: ACIDS ENCODI FILE REFERENCE: P333021C59	1554 TGTACAGACACATTTGGCAAAGAAGTAGATTTGGCCCTTCAGAATGTTATTCTCACCTT 1613
	1494 CCGTGTGGACTGAATCAATGGATCTGTATAGATGGGTTTGTATGAGTGGGGATAACAA 1553 
APPLICANT: Goddwart, Paul J. APPLICANT: Goddwart, Paul J. APPLICANT: Gurney, Austin L. APPLICANT: Sherwood, Steven APPLICANT: Smith Victoria	1434 GAATATTGCAATGGATCATCTGCATCATGCCCAGAAACCACTATGTTCAGACTGGGCAT 1493 
	1377 CTATTTATGTCAAAAGAATGTGTAGGCCTTCCTTTGAAGAATGCGACCTCCCT 1433 418 GluLeuSerIleAlaGlyThrProCy8ArgLy8SerIleAspProGluCy8AspPheThr 437
APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen APPLICANT: Descript, Jaura APPLICANT: Descript, Laura APPLICANT: Descript, Laura	1320 ACATGTAGATTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGCGAAAACTGT 1376        :::     
KESULT 13 US-10-140-002-204 ; Sequence 204, Application US/10140 ; Patent No. 6725730 GENERAL INFORMATION	1260 TGTGACTGTGCGACTGAACAGGATTGTGCCCTTATTGGAGAACATGCTGTGATATTGCC 1319
Db 705 SerValValSerGluSerAepA	1200 GATCCTTTTTCAAACAGCAAGCAGTGTGTGAATGCAAAGCTGGAAGCAGGAGGGG 1259 
685	1140 GACTTTGCACATTTATTTCAAAGCACAAAGTCCCAGTGTCTTCACAATCAGCCTCGCTTA 1199    ::: :::   :::       ::::::::        340 AspTyrArgTyrPheValSerLysPheGluThrLysCysLeuGlnLysLeuSerAsnLeu 359
899	1080 ATGAATCCAGAAGCAATTCATTTCAGTGGTGAGAGTCTTTAGTAACTGCAGCTTCGAA 1139 
2079	1020 AGTATGGGGATCACTTATGATGACATAATGCCAGTGCTCAGGAGCTGTCTGCATT 1079
OV 2079 CCTGAAAGGCGCTACATTGAGA	

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TTCTTTATTATTTTCTGTGTACTGATTGCTATAATGGTG 2189
                                                                                                 CATTGAGAACATTTACCATTCCAAACCAATGAGATGG------ 2129
                 ;------CTGCGGATGGACAGTAATTTTGATAGTTTA 137
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LABDValllePheHisProGluGlyGluPheAspSer--- 40
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GGAGGTGTTGTTCTGCACCCCAGAACCATAAGTCTGGAATCACTTGCAGTTATTTTAGCT 1004
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                                                                                                                   341 HisGluLeuGlyHisThrLeuGlyMetGlnHisAspGlu---GluPheCysPheCysGly
 AATATTACAATTATTCTGTCTTCATTGGAGCTTTGGATAGATGAAAATTACAACC
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                                                                      LysvalGlnGluAspvalPheLeuValValAsnIleValAspSerMetTyrGlnGlnLeu
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                                                                             GENERAL INC. 03.939.939.
FERENTAL INCRMATION:
TITLE OF INVENTION: SVPHI-8 DNA and Polypeptides
FILE REFERENCE: 03.260.0050-003.04
CURRENT APPLICATION NUMBER: US/09/617,145
FUNE REPLING DATE: 2000-07-14
PRIOR FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTING DATE: 1998-01-14
INUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTING DATE: 1998-01-14
INUMBER OF SEQ ID NOS: 2
SEQ ID NOS: 2
ILENGTH: 722
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Matches:
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TrpGly1leAspTyrHisLeuArgMetAsnIleSerAspIleGlyGlu-------
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Fatent No. 6680189
GENERAL INFORMATION:
APPLICANT: YOSHIMURA, Koji
APPLICANT: VOSHIMURA, Koji
APPLICANT: HIXICHI, Yuichi
APPLICANT: HIXICHI, Yuichi
APPLICANT: HIXICHI, Yuichi
TITLE OF INVENTION: No. 6680189el Protein and DNA Thereof
FILE REFERENCE: 2544 USOP
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: DCT/JP99/04766
PRIOR PLING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: JP 10-250115
PRIOR PLING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 32
SOFTWARE RECEIN VERSION 3.0
SEQ ID NO 15
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OTHER INFORMATION: An isolated ADAM family protein
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ORGANISM: Homo sapiens
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US-09-786-256C-15
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                                                                                  216 GTAATIGAAGGGAAACCATATACTGTGAATTTAATGCAA---AAAAACTTTTTACCCCAT 272
                                                                                                                                                                                    273 AATTTTAGAGTTTACAGTTATAGTGGCACAGGAATTATGAAACCACTTGACCAAGATTTT 332
                                                                                                                                                                                                                     :::
82 GlyTyrThrGluThrTyrTyrAsnSerThrGlyLysGluIleThrThrSerProGlnIle 101
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| ProLeuSerProlleHisArgAspGlyGlnGluHisAlaLeuPheLysTyrAsnProAsp 161
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162 GluLysAsnTyrAspSerThrCysGlyMetAspGlyValLeuTrpAlaHisAspLeuGln 181
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-GlnGluGlnPheGluThrGluLeuLysTyrLysMet 61
                                                                                                                CAGAATTTCTGCCACTACCAAGGGTATATTGAAGGTTATCCAAAATCTGTGGTGATGGTT
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                                  1245 GAAGCAGAGAGGAGTGTGACTGTGGGACTGAACAGGATTGTGCCCTTATTGGAGAAACA 1304
                                                                                                    TGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGC 1364
                                                                                                                                                                        GACCTCCCTGAATATTGCAATGGATCATCTGCCATCATGCCCAGAAAACCACTATGTTCAG 1484
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                                                     552 IleProCysLysAlaAsnAspThrMetCysGlyLysLeuPheCysGlnGlyGrAsp 571
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617 CysValAspIleGluLysAlaTyrLysSerThrAsnCysSerSer---LysCysLysGly 635
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                                                                                                                                     433 CysCysAspAlaLysThrCysLysIleLysAlaThrPheGlnCysAlaLeuGlyGluCys 452
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; Publication No. US20030044813A1
; GENERAL INFORMATION:
; APPLICANT: Old, Lloyd J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Cancer-Testis Antigens
; FILE REFERENCE: LO461/7125 (JRV)
; CURRENT APPLICATION NUMBER: US/10/054,683
; CURRENT PILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/280,718
; PRIOR PILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/285,154
; PRIOR APPLICATION NUMBER: US 60/285,154
; PRIOR APPLICATION NUMBER: US 60/285,154
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; SEQ ID NO 19
; LENGTH: 734
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-MODEL=frame+ nzp.model - DEV=Xlp
-MODEL=frame+ nzp.model - DEV=Xlp
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-LCOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=b)csumc2
-TRANS=human+0 - Cdi - LLIST=445 - DOCALIGN=200 - THR SCORE=pect - THR MAX=100
-THR MIN=0 - ALIGN=15 - MODEL=LOCAL - CUTFMT=pect - NORM=ext - HEAPSIZE=500 - MINLEN=0
-MAXLEN=200000000 - USER=US10054683 @CGN | 1 1 393 @runat 10012005_174512_15537
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-LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                  - protein search, using frame_plus_n2p model
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Database

Result

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APPLICANT: OLD, Lloyd
APPLICANT: SCANLAN, Matthew
APPLICANT: CHEN, Yao-Tseng
TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
FILE REFERENCE: L0461.70155US00
CURRENT APPLICATION NUMBER: US/10/473,603
CURRENT APPLICATION NUMBER: DCT/USO2/09808
FRICA APPLICATION NUMBER: PCT/USO2/09808
FRICA APPLICATION NUMBER: DCT/USO2/09808
FRICA APPLICATION NUMBER: 00/209.718
FRICA PAPLICATION NUMBER: 60/280,718
FRICA APPLICATION NUMBER: 60/280,718
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Sequence 19, Application US/10473603 Publication No. US20040235066A1 GENERAL INFORMATION:

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969 ACCATAAGTCTGGAATCACTTGCAGTTATTTAGCTCAATTATTGAGCCTTAGTATGGGG 1028	49 CATTTATTCAAAGCAGAAGTCCCAGTGTCTTCACAATCAGCCTCGCTTAGATCCTTTT 12	ALINALAVAILYBGIJABINALALYBENGGIUALAGIJVIUGIUCYBABĒCYS 40 CAGGATTGTGCCCTTATTGGAGAACATGCTGTGATATTGCCACATGTAGA 13 	TCAAACTGTGCTGAAGGACCATGCTGCGAAAACTGTCTATTTAT 	441 LysGluArgMetCysArgProSerPheGluCysAspLeuProGluTyrCysAsnGly 460 1449 TCATCTGCATCATGCCCAGAAACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAAT 1508	09 CAATGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACATTT 156	AAGAAGTAGAGTITGACCCTTCAGAATGTTATTCTCACCTTAATTC 		VIII 	gcagacagcaaaagatgtggataaaagatggaacttcttg 	869 TGCAGGAATCAAAGATGTGAGTTCTTCATACTTGGGTTATGATTGTACTACTGACAAA 192 	929 IGCANIGATRAGAGGICIATIGCAATAACAAAAAGCACTGITGTGGTGCTTCATATTTA 198. 621 CY8A8IA8BPATGGIYVALCY8A8IA8GABTGIY8H18CY8H18CY8H18CY8ASEATAYTACU 640	1989 CCTCCAGATTGCTCAGTTCAATCAGATCTATGGCCTGGTGGGAGTATTGACAGTGGCAAT 2048 
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<pre>     TYPE: PRT     ORGANISM: Homo sapiens     US-10-205-823-8  Alignment Scores:     Dred. No.:     Score:     Score:</pre>	72 ATGTGGGTCTTGTTTCTGCTCAGGGGCTCGG	21 AspSerLeubrovalGinileThrValProGluLysileArgSerileIllIIII	30	### STATE CANDERS TO STATE TO	GAAAATGTTAGTTATGGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAACATGTAATT 48	9 TACCAAGTAAAACATAAGAAAGCAGATGTTTCCTTATATAATGAGAAGGATATTGAATCA 54 	549 AGAGATCTGTCCTTTAAATTACAAAGGGCAGAGCCACAGCAAGATTTGCAAAGTATATA 608 [	CLUMECALBVAILLEVAIGLULYBGINLEULYTABRHISMECGIYSERASPINTI GTCGCTCAAAAAGTTTTCCAGTTGATTGACGAATGCTATTTTGTTTCAI	CCACT 78       hrThr 24	rrrra       alteu	849 CGTCCTCATGATGTGGCATTTTTACTTGTTACAGAGAAAAGTCAAATTATGTTGGTGCA 908 	909 ACCTITCAAGGAAGAIGIGIGAIGCAAACTAIGCAGGGAGGAGTIGIICIGCACCCCGGA 968 

165 ATACGGTCAATAATAAAGGAATTGAATCGCAGGCATCCTACAAAATTGTAATTGAA 22	111 HistyrdinglyfyrliedludiyfyrProLysSerValvalMetValserThrCysThr  405 GGACTCAGGGGCTACTACAAATGTACTAGTATAGAATACAACCCCTGGGGTCT  131 GlyLeuArgGlyValLeuGlnPheGluAsnValSerTyrGlylleGluProLeuGluSer  465 TCACTTGGCTTTGAAATTTACCAAGTAAAACATAAGAAAGCAATGTTTCCTTA  151 SerValGlyPheGluHisValIleTyrGlnValLysHisLysLysAlaAspValSerLeu  525 TATAATGACAAGATATTACAACAAGTAAAACATAAGAAACAATTGTATAAT  171 TyrAsnGluLysAspIleGluSerArgAspLeuSerPheLysLeuGlnSerValGluPro  585 CAGCAAGATTTTGCAACAAGTAATTAGAAAACATTGAAAACAATTGTATAAT  191 GlnGlnAspPheAlaLysTyrIleGluMetHisValIleValGluLysGlnLeuTyrAsn  645 CATATGGGGTCTGATACAACTGTTGTGTAAAAACAATTGTAATAA  106 GlnGlnAspPheAlaLysTyrIleGluMetHisValIleValGluLysGlnLeuTyrAsn  647 GATGAAAAATTGTAAAAATTACAATTATTCTGTCTTCATTGGATTGATT	Db 291 GluiysserksnityrvalGlyAlaThirPheGlnGlyLysMetCysAspAlaAsnityrala 310  Qy 945 GGAGGTGTTGTCTCCCCCAGAACCATAAGTCTGGAATATTTTACT 1004
Oy 2049 TTTCCACCTGTAGCTATACCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTAC 2108	SULT 5  SULT 5  SQUARES 2.6  Sequence 6, Application US/10205823  SPELICANT: Schagel, Kobert  APPLICANT: Schagel, Walson O.  APPLICANT: Bndege, Wilson O.  APPLICANT: Gorbaccheva, Bella  APPLICANT: Gorbaccheva, Bella  APPLICANT: Gorbaccheva, Sebastian  APPLICANT: Karen  APPLICANT: Karen  APPLICANT: Momesy, Angela M.  APPLICANT: Momesy, Angela M.  APPLICANT: Angela M.  APPLICANT: Angela M.  APPLICANT: Alexan  APPLICANT: Alexan  APPLICANTON: NOVEL GENES, COMPOSITIONS, KITS, AND  TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT  TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  FILE REFERENCE: MRI-044  CURRENT APPLICATION NUMBER: 60/307, 982  PRIOR PILING DATE: 2001-07-25  PRIOR PLING DATE: 2001-07-25  PRIOR PLING DATE: 2001-08-25  PRIOR PLING DATE: 2001-08-25  PRIOR PLING DATE: 2001-10-25  PRIOR PLING DATE: 2001-03-05  RUMBER OF SEC ID NOS: 455  SOFTWARE FEALSCO FOR Windows Version 4.0	### PENGTH: 753 ### PENGTH: 75

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LENGTH: 820
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 2, Application US/09961656
Publication No. US20030017572A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: Sidos-Santiago, Inmaculada
APPLICANT: Sapeller-Libermann, Rosana
TITLE OF INVENTION: S6224, 56629, NOVEL HUMAN
TITLE OF INVENTION: METALLOPROTEASES AND USES THEREOF
FILE REFRENCE: 10448-092002
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/235,035
PRIOR APPLICATION NUMBER: 60/235,035
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTERE FOR Windows Version 4.0
FENCH APPLICATION NOWER 12000-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTERE FASTERE
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APPLICANT: Desnoyers, Luc
APPLICANT: Godaadd Audrey
APPLICANT: Godaadd Audrey
APPLICANT: Godaadd Audrey
APPLICANT: Godawski, Paul J.
APPLICANT: Godwwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victorian L.
APPLICANT: Smith, Victorian L.
APPLICANT: Smith, Victorian L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mod, William I.
APPLICANT: Modod, William I.
APPLICANT: MODOD SECOLOBER
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT APPLICATION NUMBER: 60/662287
PRIOR FILING DATE: 1997-00-17
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
                                                                                             1767 ATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGTGATCATGCAGACAGCCAAAAG 1826
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|ProAlaValProAgpLeuPheProLeuTyrLeuGlumetHisIleValValAspLysThr 230
                                                                  CTTTGGATAGATGAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACACACA 815
                                                                                                                                                                                        PheLeuGluTrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeu 310
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                                                                                                          GGATTGACGAATGCTATTTTTTTTTTTAATATTACAATTATTCTGTCTTCATTGGAG 755
                                                TIGTATAATCATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTCCAGTTGATT
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NUMBER: 60/069873 1997-12-17 NUMBER: 60/078910 1998-03-25 NUMBER: 60/07954 1998-03-25 NUMBER: 60/079566 11998-03-27 NUMBER: 60/07978 11998-03-17 NUMBER: 60/081819 11998-03-17 NUMBER: 60/081955 11998-04-15 NUMBER: 60/081819 11998-04-15 NUMBER: 60/081819	74-22 55-06 (08444) 55-06 (08532) 55-15 (0708557) 55-15 (0708953) 60 (08953) 60 (08990) 60 (08990)	NUMBER: 60/09516 1998-08-10 1998-08-11 NUMBER: 60/096791 1998-08-17 NUMBER: 60/09586 1998-08-31 NUMBER: 60/098544 1998-08-31 NUMBER: 60/09859 1998-09-09 NUMBER: 60/09989 1998-09-10 NUMBER: 60/09981 1998-09-10 NUMBER: 60/09981 1998-09-10 NUMBER: 60/09981 1998-09-10 NUMBER: 60/099816 1998-09-10 NUMBER: 60/0938 1998-09-10 NUMBER: 60/10038 1998-09-11 NUMBER: 60/10038 1998-09-11 NUMBER: 60/10038 1998-09-11 NUMBER: 60/10038 1998-09-15 NUMBER: 60/10038
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PRIOR PLING DATE: 1998-09-18
PRIOR PLING DATE: 1998-09-18
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PRIOR PLING DATE: 1998-09-18
PRIOR PLING DATE: 1998-09-24
PRIOR PELING DATE: 1998-09-25
PRIOR PELING DATE: 1998-09-25
PRIOR PELING DATE: 1998-09-25
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301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
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                                                                                                AATGCTATTTTTGTTTCATTTAATATTACAATTATTCTGTCTTCATTGGAGCTTTGGATA
                                                                                                               GATGAAAATAAAATTGCAACCACTGGAGAGAGCTAATGAGTTATTACACACATTTTTAAGA
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SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln
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LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe
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Matches:
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R APPLICATION NUMBER: 60/146963

R FILING DATE: 1999-08-03

R FILING DATE: 1999-08-03

R FILING DATE: 1999-08-17

R APPLICATION NUMBER: 60/149320

R FILING DATE: 1999-08-17

R APPLICATION NUMBER: 60/15733

R FILING DATE: 1999-08-17

R FILING DATE: 1999-08-31

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                                                     APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
APPLICATION NUMBER: 60/146222
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APPLICATION NUMBER: 60/166361
FILING DATE: 1999-11-16
APPLICATION NUMBER: 60/169445
FILING DATE: 1999-12-07
APPLICATION NUMBER: 60/141037
FILING DATE: 1999-06-23
APPLICATION NUMBER: 60/144758
FILING DATE: 1999-07-20
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APPLICATION NUMBER: 60/100627
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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Geartien, Mary
APPLICANT: Godward, Audrey
APPLICANT: Godward, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: BOOG, William I.
APPLICANT: APPLICATION NUMBER: 10/119, 480
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-18
PRIOR PILING DATE: 1997-10-31
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Publication No. US20030036635A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/07928
PRIOR APPLICATION NUMBER: 60/08199
PRIOR APPLICATION NUMBER: 60/08199
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
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PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-12
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08532
PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08953
PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08953
PRIOR PELING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09059
PRIOR PELING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09059
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09059
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09059
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-08-10
PRIOR PELING DATE: 1998-08-17
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
R RAPLICATION NUMBER: 60/079656
R FILING DATE: 1998-03-26
R R FLING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079728
R FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1938-09-09
PRIOR PELLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10
PRIOR PPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099816
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APPLICATION NUMBER: 60/100038
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FILING DATE: 1998-09-15
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98-09-16 98-09-18 98-09-18 98-09-19 98-09-17 98-09-17 BER: 60/101477 98-09-24 98-09-24 98-09-24 98-09-24 98-09-24 98-09-24 98-09-24 98-09-25	RE 60/10617 RE 60/10617 RE 60/10624 FRE 60/10646 FRE 60/10646 FRE 60/10690 FRE 60/10890 FRE 60/10890 FRE 60/10890 FRE 60/10890 FRE 60/11329 FRE 60/11329	01.0
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GENERAL INCOMMATION

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerriteen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Matanabe, Colin L.

APPLICANT: Matanabe, Colin L.

APPLICANT: Mood, William I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: 19330PL02

CURRENT APPLICATION NUMBER: US/10/230,338

CURRENT FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-0-17

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PRIOR APPLICATION NUMBER: 60/06349

PRIOR FILING DATE: 1997-10-21

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-26
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TYPE: PRT
CORGANISM: Homo Sapien
US-10-218-631-90
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APPLICANT: Geritteen, warry
APPLICANT: Goddard, Audrey
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PL04
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PL04
CURRENT APPLICATION NUMBER: 10/119, 480
PRIOR FILING DATE: 1002-04-09
PRIOR FILING DATE: 1097-09-17
PRIOR FILING DATE: 1097-10-17
PRIOR PILING DATE: 1097-10-28
PRIOR FILING DATE: 1097-10-31
PRIOR PILING DATE: 1097-10-31
PRIOR PILING DATE: 1097-12-17
PRIOR APPLICATION NUMBER: 60/069973
PRIOR PILING DATE: 1099-10-30
PRIOR PILING DATE: 1099-03-26
PRIOR FILING DATE: 1099-03-26
PRIOR FILING DATE: 1099-03-26
PRIOR FILING DATE: 1090-03-26
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578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
                                 GATGGAACTTCTTGTGGTTCAATAAGGTTTGCAGGAATCAAAGATGTGTGAGTTCTTCA
                                                     TACTTG------GGTTATGATTGTACTACTGACAAATGCAATGATAGAGGTGTATGC
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Garritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe
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PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 90
LENGTH: 787
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: BAREAL NEW, INC.
APPLICANT: Goddard, Auduri P.
APPLICANT: Goddard, Auduri J.
APPLICANT: Goddard, Auduri J.
APPLICANT: Goddard, Auduri J.
APPLICANT: Goddard, Austin L.
APPLICANT: Ginneld, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Watenabe, Colin L.
APPLICANT: Word Milliam I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT PRILING DATE: 2002-08-28
FRIOR PELING DATE: 1907-10-17
FRIOR APPLICATION NUMBER: 60/059113
FRIOR APPLICATION NUMBER: 60/059113
FRIOR APPLICATION NUMBER: 60/05349
FRIOR PILING DATE: 1997-10-17
FRIOR PILING DATE: 1998-03-26
FRIOR APPLICATION NUMBER: 60/079294
FRIOR PILING DATE: 1998-03-25
FRIOR PILING DATE: 1998-03-26
FRIOR PILING DATE: 1998-03-25
FRIOR APPLICATION NUMBER: 60/07928
FRIOR APPLICATION NUMBER: 60/07928
FRIOR APPLICATION NUMBER: 60/07928
                                        1950 AATAACAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCAGATTGCTCAGTTCAA 2009
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       618 IlelleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
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SEQ ID NO 90
LENGTH: 787
TYPE: PRT
ORGANISM: Homo Sapien
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Publication No. US20030050448A1
GENERAL INFORMATION:
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341 GluserThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
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|LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys
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LeuTrpLeu-----LeuLeuAlaGlyLeuCygGlyLeuLeuAlaSerArgProGlyPhe
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Db 657 Ser 671	OY 2058 GTAGCTATACCAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCATTCCAAA 2117	ylysThr	Oy 2118 CCAATGAGATGACCATTTTTTTTTTTTTTTTTTTT	Qy 2172 CTGATTGCTATAATGTGAAAGTTAATTTCCAAAGGAAAAATGGAGAGCTGAGGACTAT 2231		715	78-10-232-224-90 7. Sequence 90, Application US/1023224	; Publication No. US20030065147A1 ; GENERAL INFORMATION: : APPLICANT: Baker, Kevin P.			; APPLICANT: Stephan, Jean-Philippe F. ; APPLICANT: Watanabe, Colin L. ; APPLICANT: Wood, William I. ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	; TITLE OF INVENTION: ACIDS ENCODING THE SAME ; FILE REPERENCE: 933:091C111 ; CURRENT APPLICATION NUMBER: US/10/232,224 ; CURRENT FILING DATE: 2002-08-29	; PRIOR APPLICATION NUMBER: 10/119,480 ; PRIOR FILLING DATE: 2002-04-09 ; PRIOR APPLICATION NUMBER: 60/059113 ; PRIOR FILLING DATE: 1997-09-17	; PRIOR APPLICATION NUMBER: 60/062287 ; PRIOR FILING DATE: 1997-10-17 ; PRIOR PLILING DATE: 1997-10-28		APPLICATION NUMBER: FILING DATE: 1998-03 APPLICATION NUMBER: FILING DATE: 1998-03	; PRIOR APPLICATION NUMBER: 60/079656 ; PRIOR FILING DATE: 1998-03-26 ; PRIOR APPLICATION NUMBER: 60/079728 ; PRIOR PLILING DATE: 1998-03-27	Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246 SEQ ID NO 90 LENGTH: 787	; TYPE: PRT ; ORGANISM: Homo Sapien US-10-232-224-90	6 Length: Matches:	t Similarity: 58.89% ocal Similarity: 41.11% Match: 31.79%

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FILE PREFERENCE: P3530PIC6
CURRENT APPLICATION NUMBER: US/10/216,159A
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06513
PRIOR FILING DATE: 1997-10-17
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Watanabe, Colin L.
Wood, William I.
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
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361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyVallysCysLeuGln 380
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129 GATAGTTTACCTGTGCAAATTACAGTTCCGGAGAAAATACGGTCAATAATAAGGAAGG	0 0	GTGAATTTAATGCAAAAAACTTTTTACCCCATAATTTTAGAGTTTACAGTTATAGTGGC	62 ValhisLeuLysGinArgTyrPheLeuAlaAspAsnPheMetlleTyrLeuTyrAsn 80 300 ACAGGAATTATGAACCACTTGACCAGATTTTCAGAATTTCTGCCACTACCAAGGTAT 359	81 GlnGlyserMetAsnThrTyrSerSerAspilleGlnThrGlnCysTyrTyrGlnGlyAsn 100	Allemodifalcommanicierosicalesitacendistricesticadococcia 	420 CTACAGTTTGAAAATGTTAGTATAGGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAA 479	CATGTAATTTACCAAGTAAAACATAAGAAAGCAGATGTTTCCTTATATAATGAGAAGGAT	141 HisValLeuTyrLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160 540 ATTGAATCAAGAGATCTGTCCTTAAATTACAAAGCGCAGAGCCACAGCAA 590	161 LeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal 180	591 GATTITGCAAAGTATATAGAAATGCATGTTATAGTTGAAAAACAATTGTATAAT 644  181 ProAspLeuPheProLeuTyrLeuGluMetHislleValValAspLysThrLeuTyrAsp 200	CATATGGGGTCTGATACAACTGTTGTCGCTCAAAAGTTTTCCAGTTGATTGGATTGACG	201 iyrirpGiyserAbpserMetileValihrAbniy8ValileGiulleValGiybeuAla 220 705 AATGCTATTTTTGTTTCATTTAATATTACAATTATTCTGTCTTGAGGGGTTTGGATA 764	::::::       :::      :	765 GATGAAAATAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACACACATTTTTAAGA 824	825 TGGAAAACATCTTATCTTTTACGTCCTCATGATGTGGCATTTTTACTTGTTTACAGA 884	GAAAAGTCAAATTATGTTGGTGCAACCTTTCAAGGAAGATGTGTGATGCAACTATGCA	281 ASPLYIFICALGLYIDEUGLYALGVALAVAIFHEFIOGLYIHIRGECLYBLIEHHANGLYISSEL 300 945 GGAGGTGTTGTTCTGCACCCCAGAACCATTGGAATCACTTGCAGTAATTTTAGCT 1004	301 AlaGlyValAlaLeuTyrProLygGlulleThrLeuGluAlaPheAlaValIhr 320	1005 CAATTATTGAGCCTTAGGAGGATCACTTATGATGACATTAACAAATGCCAGTGCTCA 1064    :::   :::    :::	1065 GGAGCTGTCTGCATTATGAATCCAGAAGCAATTCATTTCAGTGGTGTGAAGATCTTTAGT 1124	1125 AACTGCAGCTTCGAAGACTTTTGCACACTTTTATTTCAAGCAGAAGTCCCAGTGTTTTATTCAAGCAGAAGTCCCAGTGTCTTTCACTTTTATTTCAAGAGAAGTCCCAGTGTCTTTCACTTTTATTTCAAGAGAAGTCCCAAGTGTCTTTCACTTTTATTTCAAGAGAAGTCCCAAGTGTCTTTCACTTTTATTTCAAGAGAAGTCCCAAGTGTCTTTCACTTATTTCAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAAAA	361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380 1185 AATCAGCCTCGCTTAGATCCTTTTTCAAACAGCAAGCAGTGTGTGT
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AGTGCGGAAAATTAATATGTAAATATGTA 1718 |||||||:::|||| || 1eCysGlyArgLeuValCysThrTyrPro 557 CATATTTACCTCCAGATTGCTCAGTTCAA 2009 CCGGTTCAAACTGTGCTGAAGGACCATGC 1364 SAATGTGTAGGCCT---TCCTTTGAAGAA 1421 ||||||||||| alGluCy8ArgProLy8AlaHi8ProGlu 457 GGARCTGTATAGATGGAGTTTGTATGAGT 1541
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helleCysTyrAspGlyAspCysHisAsp 497 CTATTATTTATGCCAACATAAGTGGACAT 1778 ------GACAGTGGCAATTTTCCACCT 2057 SCTACATTGAGAACATTTACCATTCCAAA 2117 TCATICCITICITIATIATITICIGIA 2171 AAAGGAAAAATGGAGAACTGAGGACTAT 2231 AACAGGATTGTGCCCTTATTGGAGAACA 1304 TIGCATCATGCCCAGAAACCACTATGTT 1481 AAGAAGTAGAGTTTGGCÇÇTTCAGAAŢĢŢ 1601 CTGGAAACTGTGGTATAAGT---GATTCA 1658 ATGCAGACAGCCAAAAGATGTGGATAAAA 1838 SCAGGAATCAAAGATGTGTGAGTTCTTCA 1898 ||| |||::: roglugluAspMetGlySerIle----- 671 uAlaGlnCysGly-----ProAlaSer 417 heGlyAanCysGlyArgAspArgAsnAsn 537 :::|||||||||||| spvallieTyrAlaPhevalArgAspSer 577 ::: |||| rgThrValProAspProLeuAlaValLys 597 :::||| ----MetGluArgAlaSerGlyLysThr 679 :::||| |aleuProlleLeulleVal------ 696 rolysProValCysGlyAsnGlyArgLeu 399 || ||||||||| |nLeuLysLysTrpPheAlaLysGlu--- 714 AACCTAAAGGG 2273

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945 GGAGGTGTTGTTGTGCACCCCGAGAACCATAAGTCTGGAATCACTTGCAGTTATTTTAGCT 1004
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                                                                                            181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThrLeuTyrAsp 200
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361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
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 ATTGAATCAAGA-----GATCTGTCCTTTAAATTACAAAGCGCAGAGCCACAGAAA 590
                                                                                                                                                  CATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTTCCAGTTGATTGGATTGACG 704
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Serphan, Jean-Philippe F.
APPLICANT: Serphan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPL
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LeuTrpLeu-----LeuLeuAlaGlYLeuCygGlYLeuLeuAlaSerArgProGlyPhe
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-----GluGluPheProSerSerGluSerLysSerGluGly 726
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                                                                     Sequence 90, Application US/10218849
Publication No. US20030073814A1
GENERAL INFORMATION:
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090691

R APPLICATION NUMBER: 60/090695

R APPLICATION NUMBER: 60/091695

R APPLICATION NUMBER: 60/091982

R APPLICATION NUMBER: 60/091982

R APPLICATION NUMBER: 60/091982

R APPLICATION NUMBER: 60/095302

R APPLICATION DATE: 1998-08-04
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R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/081819
R FILING DATE: 1998-04-15
R FILING DATE: 1998-04-15
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/08905
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090557
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RFILING DATE: 1998-08-04
RR APPLICATION NUMBER: 60/095916
RFILING DATE: 1998-08-10
RR APPLICATION NUMBER: 60/096146
RFILING DATE: 1998-08-11
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PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099811
FILING DATE: 1998-09-10
                                                  ILING DATE: 1997-10-28
PLICATION NUMBER: 60/064103
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APPLICATION NUMBER: 60/069873
FILING DATE: 1997-12-17
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APPLICATION UNMBER: 60/08441
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/085323
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FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-09-09
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APPLICANT: Gerriteen, Mary
APPLICANT: Gedard, Audrey,
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Victoria L.
APPLICANT: Suphan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330P1C72
CURRENT FILING DATE: 2002-08-26
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/05287
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                                                                                              538 LysTyrValPheCysGlyTrpArgAsnLeulleCysGlyArgLeuValCysThrTyrPro 557
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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OM protein - protein search, using sw model

Run on:

January 10, 2005, 21:47:51; Search time 160 Seconds (without alignments) 1645.671 Million cell updates/sec

Title: Perfect score:

US-10-054-683-19 3984 1 MWVLFLLSGLGGLRMDSNFD......WRTEDYSSDEQPESESEPKG 734 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseq11980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003s:\* geneseqp2003bs:\* geneseqp2003bs:\* A Geneseq 23Sep04:\* Database :

Pred. No. is the number of results predicted by chance to have and score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aar87037 Human PH3	Abj19246 Human can	Adb75186 Prostate	Adb75184 Prostate	Adb75182 Prostate	Aar87034 Human PH3	Aar87036 Mouse PH3	Aau83636 Human PRO	Abu80783 Human PRO		Novel	Human	Abj72400 Human PRO	Abo34295 Human sec	Abj72102 Human mem	Novel ]	Adb80686 Novel hum	Adb73227 Novel hum	Adb78309 Novel hum	Adb84957 Human PRO	Adb78063 Novel hum	Adb87129 Human PRO	Adb84711 Human PRO	Adb83826 Novel hum	Adb72981 Novel hum	
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## ALIGNMENTS

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Human PH30 beta chain sperm protein; contraceptive;
FEE integrin binding domain.
                                                                                              84. .734
/note= "see AAR87035"
                                            Human PH30 beta chain sperm protein.
                                                                                       Location/Qualifiers
      AAR87037 standard; protein; 734 AA.
                                                                                                                                                                                Alves K, Gupta SK, Hollis GF;
                                                                                                                                           95WO-US007295.
                                                                                                                                                       94US-00264101
                               30-SEP-1996 (first entry)
                                                                                                                                                                   (MERI ) MERCK & CO INC.
                                                                                                                                                                                            WPI; 1996-058212/06.
N-PSDB; AAT07328.
                                                                                                                                                       20-JUN-1994;
                                                                                                                                           06-JUN-1995;
                                                                           Homo sapiens
                                                                                                                  WO9535118-A1
                                                                                                                              28-DEC-1995.
                  AAR87037;
                                                                                        Key
Region
AAR87037
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Human and mouse sperm protein PH30 beta chain and related DNA - useful in contraceptive vaccines.

Example 2; Page 45-48; 85pp; English.

Human PH30 beta chain sperm protein, having a FEE integrin binding domain, is 58.9% identical to mouse and 56.5% identical to guinea pig PH30 beta. The protein may be produced recombinantly and used in a contraceptive composition containing an effective adjuvant and an amount of sperm protein which is effective for the stimulation of antibodies which bind to sperm protein in vivo, thereby preventing or substantially reducing the rate of sperm-egg fusion

Sequence 734 AA;

us-10-054-683-19.rag

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Diagnosing cancer comprises contacting a biological sample isolated from a subject with an agent that specifically binds to a nucleic acid molecule, its expression product or fragment or an antibody that binds to the product or fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a method for diagnosing cancer, the method involves detecting the DNA or protein sequences of human cancer/testis (CT) antigens that are disclosed in the invention. The method of the invention is useful for detecting/diagnosing, treating and monitoring a cancer or condition characterised by the expression of a human CT antigen. The present amino acid sequence represents a human CT antigen of the condition of the conditio
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 36; Page 124-126; 155pp; English.
                                                                                        30-MAR-2001; 2001US-0280718P.
20-APR-2001; 2001US-0285154P.
05-OCT-2001; 2001US-0327432P.
22-JAN-2002; 2002US-00054683.
                                                                                                                                                                                                                                                  LJ, Scanlan MJ,
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CORNELL RES
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N-PSDB; ABT15727.
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                                                      29-MAR-2002;
                  10-OCT-2002
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Human; gene therapy; vaccine; cancer; cancer/testis antigen;

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Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker CDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but
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22-MG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of sassessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 PPPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTED 720
                                                                   421 FKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLN
                                                                                                                                                                                     QWICIDGVCMSGBKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISBSGYTQCEADNL
                                                                                                                                                                                                                                                                     QCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKV
                                                                                                                                                                                                                                                                                                       QCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKWIKDGTSCGSNKV
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                                                                                                                                                   QWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL
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Anderson D;
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1, Glatt K, Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate; cancer; cytostatic; gene therapy; marker.
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
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05-MAR-2002; 2002US-0362158P
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S. Kamatkar S,
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Hoersh S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal control and cancer, and may be useful in gene therapy. Sequences given in ADB7517-ADB7531 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF 119
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Anderson D;
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M, Glatt K, Zhao X,
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25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
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Hoersh S, Kamatkar S,
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Best Local Similarity
Matches 733; Conserv
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WO2003009814-A2
                                                          06-FEB-2003
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                                                                                                                                                                                                                                                                                                                ESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIEMHVIVEKQL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYSSDEQPESE 729
Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMMIKDGTSCGSNKVCRNQRCVSSS
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                                                                                                                                                                                                               LGKLYTDQDFDSLPAQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNF
                                                                                                                                                                                                                                                                       RVYSYSGTGIMKPLDQDFQNFCHYQCYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPL
                                                                                                                                                                                                                                                                                                                                ESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSVEPQQDFAKYIEMHVIVEKQL
                                                                                                                                                                                                                                                                                                                                                                                         YNHMGSDTTVVAQKVPQLIGLTNAIPVSFNITIILSSLELMIDENKIATTGEANELLHTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFISKQKSQC
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                                                                                                                                                                    Gaps
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                                                                                                                                    Length 753;
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                                                                                                                                    Score 3898; DB 7;
Pred. No. 1.8e-285;
                                                                                                                                                                 1; Mismatches
                                                                                                                                   97.8%;
                                                                                                                                                   Local Similarity 99.0
nes 718; Conservative
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                                                                                                         Sequence 753 AA;
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Human and mouse sperm protein PH30 beta chain and related DNA - useful in
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                                                                                                                                                                                                                                                                                                                                                                                                     Human PH30 beta chain sperm protein, having an FEE integrin binding domain, may be recombinantly produced by vector-mediated gene expression in host cells, preferably mammalian cells e.g. Chinese hamster ovary (CHO) cell culture. It may be used in a contraceptive composition containing an effective adjuvant and an amount of sperm protein which is effective for the stimulation of antibodies which bind to sperm protein in vivo, thereby preventing or substantially reducing the rate of sperm to in vivo, the protein is also useful for identifying small molecules that disrupt sperm-egg interaction and fertilization
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                                        an PH30 beta chain sperm protein; contraceptive; integrin binding domain.
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             chain sperm protein
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                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                    HPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFE 356
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                                                                      177 KYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKI
                                                                                                                                      DNLQCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, secreted protein, PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
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MDDFSSEEQFESESK 734
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542 VCNNKKHCHCKSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPM
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                                                                                                                                                                                   RWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYSSDEQPESEPKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse PH30 beta chain sperm protein; contraceptive;
QDE integrin binding domain.
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/note= "see AAR87035"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                SCSLRSFQNFISNVGVKCLQNKPQMQK-KSPKPVCGNGRLEGNEICDCGTEAQCG--PAS
                                                                                                                                                                                                                                                                                                                                                 CCDFRICVLKDGAKCYKGLCCKDCQILQSGVECRPKAHPECDIAENCNGSSPECGPDITL
                                                                                                                                                                                                                                                                                                                                                                                                                          DENKI ATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYA
                                                                                                                                                           292 GGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFS
                                                                                                                                                                                                                                        NCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGET
                                                                                                                                                                                                                                                                                                                        CCDIATCRFKAGSNCAEGPCCENCLFMSKERMCRP-SFEECDLPEYCNGSSASCPENHYV
                                                                                                                                                                                                                                                                                                                                                                                                     471 QTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYTQCEADNLOCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKWMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGTSCGSNKVCRNQRCVSSSYL---GYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQ
D--PAKYIEMHVIVEKOLYNHMGSDTTVVAOKVFOLIGLTNAIFVSFNITIILSSLELWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701 LIAIMVKVNFQRKKWRTEDYSSDEQPESESFKG
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01-JUN-2001; 2010WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polypeptides, encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNLMQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
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ohan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

38.3%; Score 1524.5; DB 5; Length
Best Local Similarity 41.1%; Pred. No. 4.3e-106;
Matches 310; Conservative 134; Mismatches 259; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen ME, Goddard
Smith V, Stephan JF,
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                                              25-JUL-2000; 2000US-0220664P.
26-JUL-2000; 2000US-0220664P.
26-JUL-2000; 2000US-0220666P.
28-JUL-2000; 2000US-0220893P.
28-JUL-2000; 2000US-022425P.
23-AUG-2000; 2000US-022425P.
23-AUG-2000; 2000WO-US023322.
24-AUG-2000; 2000WO-US023328.
28-NOV-2000; 2000WS-0253646P.
01-DEC-2000; 2000US-0253646P.
01-DEC-2000; 2000US-0253646P.
01-DEC-2000; 2000US-0253648P.
20-DEC-2000; 2000WS-017259.
20-DEC-2000; 2000WS-US034956.
28-PEB-2001; 2001WS-US036520.
            2000US-0220624P.
2000US-0220638P.
2000US-0220664P.
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10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liver tumor.
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DR WPI; 2003-142045/32.

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N-PSDB; ACA66885.

The hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor.

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Claim 11; Fig 90; 314pp; English.

XX

CD polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in diagnosic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU803560

CC specific cells, tassues obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
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181 PDLFPLYLEMHIVVDKTLYDYWGSDSMIVTNKVIEIVGLANSMFTQFKVTIVLSSLELWS 240
                                                                                                                                                                                                                                                                                                          301 AGVALYPKEITLEAFAVIVTQMLALSLGISYDDPKKCQCSESTCIMNPEVVQSNGVKTFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 DGTSCGSNKVCRNQRCVSSSYL---GYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQ 646
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                                                                                                                  VNIMOKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV 116
                                                                                                                                 NCSFEDFAHFISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGET 411
                                                                                                                                                                                                                                                                                                                                                                                                                                      361 SCSLRSFONFISNVGVKCLONKPOMOK-KSPKPVCGNGRLEGNEICDCGTEAQCG--PAS 417
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                                                                                                                                                                          LOFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESR---DLSFKLQSAEPQQ 173
                                                                                                                                                                                                                                   174 D--EAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWI 231
                                                                                                                                                                                                                                                                                         DENKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYA 291
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                                                                         1 MWVLFLLSGLGGLRMD-SNFDSLPVQITVPEKIRSIIKEGIE---SQASYKIVIEGKPYT
                               Gaps
                            51,
38.3%; Score 1524.5; DB 6; Length 787; 41.1%; Pred. No. 4.3e-106;
                              Conservative 134; Mismatches 259; Indels
             Similarity
                              310;
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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide encoding sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 consideration or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, blosensors or bioreactors. These are particularly useful for detecting tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour, or liver tumour, or a fumulating the proliferation of ifferentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probbes, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes, and its encoded secreted and transmembrane polypeptides,
ful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
icyte proliferation, especially for treating lung tumors, arthritis or
969
                                                                                                                                                                                                                                                                                                                                                                         antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; pericyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; cartilage disorder; sports injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
  --MERASGKTENTWLLGFLIALPILIV---
                                                                                                                                                                                                                                                                                                                                                       transmembrane protein; PRO; cytostatic;
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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  657 S---KGFSIFPEEDMGSI-
                                                                                                                                                                                                                                                                       (first entry)
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCSFEDFAHFISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGET 411
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screening libraries of human cDNA, genomic DNA or mRNA. The PRO generalso be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antianteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovacular, endothelial or angiogenic disorder in a mammal, e.g. cardiovacular, endothelial or angiogenic disorder in a mammal, e.g. cardiovacular, endothelial or angiogenic disorder in a mammal, e.g. cardiovacular, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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phan JF, Watanabe CK, Wood WI;
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Claim 11; Fig 90; 315pp; English.

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                                              AGVALYPKEITLEAFAVIVTQMLALSLGISYDDPKKCQCSESTCIMVPEVVQSNGVKTFS
                                                                                                                            CCDIATCRFKAGSNCAEGPCCENCLFMSKERMCRP-SFEECDLPEYCNGSSASCPENHYV
                                                                                                                                                                                      INGLSCKNINKFICYDGDCHDLDARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNN
                                                                                                                                                                                                                                KYVFCGWRNLICGRLVCTYPTRKPFHQENGDVIYAFVRDSVCITVDYKLPRTVPDPLAVK
                                  GGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFS
                                                                              NCSFEDFAHFISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGET
                                                                                                    SCSLRSFQNFISNVGVKCLQNKPQMQK-KSPKPVCGNGRLEGNEICDCGTEAQCG--PAS
                                                                                                                                                                        OTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO; proliferation; pericyte cell; TNP-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                  -TTAIVLARKQLKKWFAKE---EEFPSSESKSEG 726
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Smith V,
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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N-PSDB; ABT44270.
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The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TNF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation, the stimulation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.

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                      241 DENKISTVGEADELLOKFLEWKQSYLNLRPHDIAYLLIYMDYPRYLGAVFPGTMCITRYS 300
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                 SDLWPGGSI - - - - DSGNFPPVAIPARLPERRYIENIYHSKPMRW - - PFFLFIPFIIFCV
   DENKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYA
                                                                         292 GGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVÇIMNPEAIHFSGVKIFS
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human dermal fibroblast stimulation; tumour; tissue typing;
affinity purification.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                            PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence
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                                   ABJ72400 standard; protein; 787 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                          (first entry)
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                                                                                                                                              Human PRO21340 protein.
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N-PSDB; ABT44553.
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                                                                       ABJ72400;
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RESULT 13
ABJ72400
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The invention relates to an isolated mucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate full length PRO cDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNP-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful as molecular markers for protein electrophoresis polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide
         aB
chromosome identification,
   polypeptides, useful in gene therapy, in chi
chromosome markers, or in generating probes
                                                                                                  Claim 19; Fig 90; 315pp; English
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Sequence 787 AA;

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478 INGLSCKNNKFICYDGDCHDLDARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNN 537 590 DGTSCGSNKVCRNQRCVSSSYL---GYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQ 646 547 SDLWPGGSI----DSGNFPPVAIPARLPERRYIENIYHSKPMRW--PFFLFIPFFIIFCV 700 LOFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESR---DLSFKLOSAEPQQ 173 GGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFS 351 NCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGET 411 CCDIATCRFKAGSNCAEGPCCENCLFMSKERMCRP-SFEECDLPEYCNGSSASCPENHYV 470 CCDFRTCVLKDGAKCYKGLCCKDCQILQSGVECRPKAHPECDIAENCNGSSPECGPDITL 477 QTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529 GYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKWWIK 589 DENKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYA 291 61 PDLFPLYLEMHIVVDKTLYDYWGSDSMIVTNKVIEIVGLANSMFTQFKVTIVLSSLELWS VNLMOKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV D--FAKYIEMHVIVEKOLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWI 1 MWVLFLLSGLGGLRMD-SNFDSLPVQITVPEKIRSIIKEGIE---SQASYKIVIEGKPYT 51, Gaps Length 787; Query Match 38.3%; Score 1524.5; DB 6; Length Best Local Similarity 41.1%; Pred. No. 4.3e-106; Matches 310; Conservative 134; Mismatches 259; Indels 361 57 62 121 174 181 232 241 292 301 352 412 418 471 117

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Human membrane bound receptor/protein PRO21340 amino acid sequence.
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                                                                                                                    701 LIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG
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                                                                                                                                                                                                                                                                                           ABJ72102 standard; protein; 787
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2000WO-US005841.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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657 S---KGPSIFPEEDMGSI--
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ABJ72102
ID ABJ72102
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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

Desnoyers I

Baker KP, Des Grimaldi JC,

WPI; 2003-522018/49. N-PSDB; ABT43926.

Claim 11; Fig 90; 315pp; English

This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically cyoverned by information received from other cells and the immediate conversed by information is often transmitted by secretes cytotoxic polypeptides (for example mirogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agence, such as in the blocking of receptor ligand interactions. The current invention provides the amino acid with the cDNA sequences encoding them. The novel proteins of the conditocytes. The nucleic acids of the invention may have cytostatic activities through the stimulation of the manufacture of a medicament for diagnosing or treating a tumour in a manufacture of a medicament for diagnosing or treating the amino con manumal. In addition, they may be useful for measuring or detecting the amino con expression of a tumour associated gene. The present sequence is the amino

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                                                                                                                                                                                                                                                                                        51; Gaps
                                                                                                                                                                                           Length 787;
                                                                                                                                                                                      Query Match
38.3%; Score 1524.5; DB 7; Length
Best Local Similarity 41.1%; Pred. No. 4.3e-106;
Matches 310; Conservative 134; Mismatches 259; Indels
acid sequence of a human PRO protein of the invention
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                                                                                             Sequence 787 AA;
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:07:16; Search time 43 Seconds

(without alignments)

1642.398 Million cell updates/sec
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US-10-054-683-19 3984 1 MWVLFLLSGLGGLRMDSNFDWRTEDYSSDEQPESESEPKG 734	BLOSUM62 Gapop 10.0 , Gapext 0.5
Title: Perfect score: Sequence:	Scoring table: BLOSUM62 Gapop 10.

Total number of hits satisfying chosen parameters: 283416

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Maximum Match 100%
Listing first 45 s
Listing first 41 pirst 
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fertillin beta cha	fertilin beta - cr	tMDC II protein -	tMDC I protein - c	cyritestin precurs	ADAM 5 protein pre	sperm surface prot	disintegrin and me	fertilin alpha-II	fertilin alpha-I -	metalloproteinase	meltrin alpha - mo	fertilin alpha pre	monocyte surface a	catrocollastatin p	metalloproteinase	testicular metallo	disintegrin-like m	jararhagin C precu	ADAM 6 protein pre	ecarin precursor -	androgen-regulated	androgen-regulated	disintegrin-like m	disintegrin-like t	ď	halysase - Gloydiu	급	coagulation factor
SUMMARIES	ΩI	JC4861	G02937	S47656	S47645	S18968	148100	S23403	JC7850	855060	S55059	S71949	860257	149281	A60385	855270	S48160	152361	G02390	S24789	148101	A55796	S28258	S28259	165967	I65253	JC7530	JC8056	T18900	A42972
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	Length	734	735	756	736	823	777	357	655	825	905	9	903	9	826	609	617	732	814	571	735	919	116	789	670	713	610	610	952	429
ф	ery	100.0	92.6	34.7	34.3	32.4	32.3	ó.	۲.	25.9	'n.	25.5	21.5	•	٥.	19.1	8	8	8	18.1	17.8	17.8	17.5	17.5	17.4	17.4	16.6	16.4	16.1	15.5
	Score	3984	3687.5	1383.5	1365.5	1292	1288	1166	1097	1031.5	1022.5	1016.5	857	795	166	762	729	724.5	721	719.5	711	710.5	698	696.5	695	692.5	663	653.5	4	616.5
	Result No.	-	~	e	4	Ŋ	9	7	89	6	10	11	12	13		15	16	17	18	19	50	21	22	23	24	25	26	27	28	29

hemorrhagic protei atrolysin A (EC 3.	metalloproteinase metalloproteinase	ADAM 4 protein pre	disintegrin-like m atrolysin E (EC 3.	metalloproteinase-	trigramin precurso	fibrinolytic prote	trimucin precursor	hemorrhagic protei	hypothetical prote	fibrinolytic metal	atrolysin B (EC 3.	fibrolase (EC 3.4.
A37877 S41607	A59414 S48169	149283	S38539 A43296	JC8020	A30065	JC4342	843125	JQ1301	T26644	JC4880	S41608	HYSNFA
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416	419	473	524 478	484	480	481	481	478	1042	478	414	411
15.4	14.9	14.3	14.0 13.9	13.4	13.4	13.3	13.3	12.6	12.2	11.7	6.6	6.6
614.5 15.4 606 15.2												

## ALIGNMENTS

fertilin beta chain - 1 Grgefeies: Homo sapiens C.Species: Homo sapiens C.Date: 15-Aug-196 #sec C,Accession: JC4861 R:Gupta, S.K.; Alves, K Biochem. Blophys. Res. A;Title: Molecular clon. A;Reference number: JC48 A;Accession: JC4861 A;Molecula type: mRNA A;Residues: 1-734 cGUP- A;Comment: This protein C;Comment: This protein C;Superfamily: mouse me: C;Superfamily: mouse me: C;Superfamily: mouse me: F;382-734 Froduct: fert: F;48-450/Region: integ: F;48-450/Region: integ: F;686-708/Domain: transi F;121,21,219,352,458,565/B;	JC480LI 1 JC480LI MUID: 96295488; PMID: 8702389  A;Reference number: JC480LI MUID: 96295488; PMID: 8702389  A;Reference number: JC480LI MUID: 96295488; PMID: 8702389  A;Reference number: JC480LI MUID: 9629565; GB: U38805; NID: 94151118; PIDN: AAD04206.1; PID: 941511  A;Residues: 1-734 cGUP- A;Residues: L-734 cGUP- A;C00ment: This protein is an integral sperm membrane glycoprotein, and plays a role in C;Superfamily: mouse meltrin alpha; disintegrin homology climated chain # steatus predicted circal circal minestrin beach and minestrin minestrin beach and membrane protein  F;382-467/Domain: disintegrin binding # status predicted circal circa
Query Match Best Local Matches 73	Query Match Best Local Similarity 100.0%; Pred. No. 5.3e-265; Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
95 1	1 MWVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYXIVIEGKPYTVNLM 60 
Oy 61 Db 61	. OKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVNVSTCTGLRGYLQFE 120 
Qy 121 Db 121	. NVSYGIEPLESSYGFEHVIYQVKHKKADVSLYNEKDIESBDLSFKLOSAEPOODFAKYIE 180 
Qy 181 Db 181	. MHVIVEKOLYNHMGSDTTVVAQKVFOLIGLTNALFVSFNITIILSSLELMIDENKIATTG 240 
Qy 241 Db 241	EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFOGKMCDANYAGGVVLHPRT 300
Oy 301 Db 301	ISLESLAVILAQLISLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360 

361 FISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420

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A,Cross references: UNIPROT:028483; EMBL:X77619; NID:9531477; PIDN:CAA54713.1; PID:953147.
C,Superfamily: mouse meltrin alpha; disintegrin homology
F;388-473/Domain: disintegrin homology <DIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAK-- 177
                                                                                                                                                                                                                                                421 FKAGSNCAEGPCCENCLFMSQERVCRPSFDECDLPEYCNGTSASCPENHFIQTGHPCGPN 480
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                                                                                                            101 TISERSLAVILAQLESLSMGIPYDDINQCQCSAAVCIMNPEAIHFSGVKIFSNCSIEDFA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKAGSNCAEGPCCENCLFMSKERMCRPSFEEGDLPBYCNGSSASCPENHYVQTGHPCGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 KNFLPHNFRVYSYSGTGI -- MKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF
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                                                                                                                                                                                                                                                                                                                                                                      540 QCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKV
                                                                                                                                                                                                                                                                                                                                                                                            541 QCGKLICKYAGEFLLQIPRATIIYANISGHLCVAVEFASDHEDSHKWMIKDGTSCGSNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                            CRNORCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSI-IKEGIESQASYKIVIEGKPYTVNLMQ
                                                                                                                                                                         QWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL
              GEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPR
                                                                                                                                                         360 HFISKOKSOCLHNOPRLDPFFKOOAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR
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34.7%; Score 1383.5; DB 2; Length 756;
Best Local Similarity 38.1%; Pred. No. 6.6e-87;
Matches 293; Conservative 122; Mismatches 290; Indels 65;
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CiSpecies: Macaca fascioularis (crab-eating macaque)
CiDate: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
CiAccession: G02937, S550G1
A;Ramarao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-735 cRAM>
A;Residues: 1-735 cRAM>
A;Cross-references: UNIPROT:Q28478; EMBL:U33959; NID:g998339; PID:g998340
R;Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A;Reference number: S55059; MUID:95260313; PMID:7741716
A;Residues: 1-722, SS, 7724-735 cPER>
A;Cross-references: EMBL:X77653; NID:g794076; PIDN:CAA54733.1; PID:g794077
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;383-468/Domain: disintegrin homology cDIS>
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WicibGvCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ
                                                                                                                                                                                                                                                                                        RNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNF
                                                                                                                                                                                                                                                                                                                                                             KAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQ
                                                                                                                           WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLO
                                                                                                                                                                                                CGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKWWIKDGTSCGSNKVC
                                                                                                                                                                                                                                                                      RNORCVSSSYLGYDCTTDXCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNF
                                                                                                                                                                                                                                                                                                                                          PPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDY
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91.3%; Pred. No. 1.1e-244;
ive 31; Mismatches 32; Indels
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 148784; S18968
R;Senfileben: A.; Mallat, S.; Lemaire, L.; Heinlein, U.A.O.
Dev. Growth Differ. 36, 49-58; 1994
A;Title: Pre and postmeiotic germ cell specific expression of TAZ83, a gene encoding a p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 PPDCDPSMSS---PGGSIDDGFWLSVDKSVPL-FPKQRAAPK---NNGLLISFYIFSPLL 695
                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                               IHFSGVKIFSNCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGT 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 VSGNCGISDSGYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASD 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPDC--SVQSDLWPGGSIDSGNFPPV--AIPARLPERRYIENIYHSKPMRWPFFLFIPFF 695
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                                                           KFGNCG-----QRCPFFDILCGKIVCHWIHSELVPMTDLDIQYTYLGGHVCLSAH-ARN
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                                                                                                                                                                                                                                        QGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEA
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                                   LSFKLQSAEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNIT
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C;Genetics:
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C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>
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Best Local Similarity 34.2%; Pred. No. 1.4e-80;
Matches 256; Conservative 156; Mismatches 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: 148784
A;Accession: 148784
A;Statue: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-823 <RES>
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547645
tMDC I protein - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: 847645
R;Barker, H.L.; Perry, A.C.F.; Jones, R.; Hall, L.
B;Ochim. Biophys. Acta 1218, 429-431, 1994
A;Title: Sequence and expression of a monkey testicular transcript encoding tMDC I, a nd
A;Reference number: 847645; MUID:94325333; PMID:8049267
A;Recession: Superiminary
A;Molecule type: mRNA
A;Residues: 1-736 cBAR>
A;Cross-references: UNIPROT:Q28482; EMBL:X76637; NID:g535016; PIDN:CAA54085.1; PID:g535G
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;392-477/Domain: disintegrin homology cDIS>
EDFAHFISKOKSOCLHNOPRLDPFFKOOAVCGNAKLEAGEECDCGTEODCALIGETCCDI 415
                                                                                                                                                                                                                                                                                                                       420 LTCRLKDNAQCGSGDCCSKDCKFKPANTICRKSVDVECDFTEFCNGSYPYCLLDTYVRDG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: ||||:| : | : | :: || :: | CLFQHILCGKLVCTWEHKDLISRPNLSVIXAHVRDQTCVSTYLPSRKPPPVASTVSKTSY 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595 YSVDDRDETFVQDGSVCGPDMYCFKMRCKHVRFL-MDFETCEASIECSGHGICNNFNHCH 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKQSFLHPHFLVYLYNESGTLY-VDSSFSKGHCFYQGYVADIPKSAVTLRTCSGLRGLLQ 122
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                                                                                                              LHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSF 355
                                                                                                                                                                                                                                                                                                                                                                                                ATCRFKAGSNCAEGPCC-ENCLFMSKERMCRPSFE-ECDLPEYCNGSSASCPENHYVQTG 473
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293

301

241

466

526 537 581 594 631

us-10-054-683-19.rpr

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sperm surface protein PH-30 beta chain precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Date: 29-dan-1993 #sequence_revieton 29-Jan-1993 #text_change 09-Jun-2000
C;Accession: 823403; 825566
R;Blobel, C.P.; Wolfsberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
N;Title: A potential fusion peptide and an integrin ligand domain in a protein active in A;Reference number: 823403
A;Accession: 823403
A;Accession: 823403
A;Molecule type: mRNA
A;Residues: 1-357 < BLO1>
A;Cross-references: EMBL: Z11720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 5-8,'X',10-32,67-88,125-129,'X',131-134,'X',136-141,'X',143;154,'X',156-161;1
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F;5-37/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>
F;5-87/Domain: disintegrin homology <DIS>
F;5-87/Domain: transmembrane #status predicted <TMM>
                                                                       ENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLOSAEPQODFA--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595 LTTVLLPEDRDETFVEDGTICGPGQYCDKWFCKEVQFINNGSCNAEIHCQGRGICNNLDN 654
                                                                                                 294 VVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNC 353
                                                                                                                                                                                                                                                                                                                                                                                          354 SFEDFAHFISKOKSOCLHNOPRLDPFFKO----QAVCGNAKLEAGEECDCGTEQDCALI 408
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                  64 ESFLSSGSVIYFYDNRGVQRSQPLLPEMD--CSYSGYVAGFPHSRVVFATCLGLRGVIQF
                                                                                                                                                                           409 GETCCDIATCRFKAGSNCAEGPCCE-NCLFMSKERMCRPSFE-ECDLPEYCNGSSASCPE
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                                                                                                                                                      ---KYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDE
                                                                                                                                                                                                                                 NKI ATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 DTYAQNGHFCDSGGAFCFNGRCRTHDRQCQALIGGDSRGAPFACYDEVNSRGDVYGNC--
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KNFLPHNFRVYSYSGTGIMK--PLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF
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A,Cross-references: UNIPROT:Q60472; EMBL:U22060; NID:g965005; PIDN:AAA74918.1; PID:g965d
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C;Species: Cavia porcellus (guinea pig)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: 148100

R;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles,

B;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles,

A;Title: ADAM, a widely distributed and developmentally regulated gene family encoding

A;Reference number: 148100; MUID:95269891; PMID:7750654

A;Accession: 148100

A;Accession: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMMI 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDGTSCGSNKVCRNQRCVSSSYL--GYDC-TTDKCNDRGVCNNKKHCHCSASYLPPDCSV 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPSS-PGGSMDDGFWLPFDXSTPL1FKRH--GLKYKKVLLISFYILLPFLVV----LAFM 708
                        NKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGG 293
                                                                                                                                                                                 SFEDFAHFISKOKSOCLHNOPRLDPFFKOO--AVCGNAKLEAGEECDCGTEODCALIGET 411
                                                                                                                                                                                                                                                                                                                                                                                            CCDIATCRFKAGSNCAEGPCCE--NCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHY 469
                                                                                                                                                                                                                                                                                                                                                                                                                                 CCNPKDCTLIDAAQCGTGPCCDKRTCTIAERGRLCRKSKDQCDFPEFCNGETEGCAPDTK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPS-ECYSHLNSKTDVSGNCGISD 528
  ----LYNEKDIESRDLSFKLQSAEPQQ 173
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                                                                                                   3 VLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSI-IKEGIESQASYKIVIEGKPYTVNLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILHPRIISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNC
                                                                             DFAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDE
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Best Local Similarity 35.5%; Pred. No. 2.4e-80;
Matches 272; Conservative 136; Mismatches 304; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ADAMS
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>
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    ENVSYGIEPLESSVGFEHVIYQVKHKKADVS-
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A,Molecule type: mRNÅ
A;Residues: 1-835 <PBR.
A;Cross-references: UNIPROT:Q28477; EMBL:X79809; NID:g794074; PIDN:CAAS6204.1; PID:g7940
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;443-523/Domain: disintegrin homology <DIS>
F;477/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fertilin alpha-II - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S55004
B;Perry, A.C.F.; Gichuhl, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A;Reference number: S55059; MUID:95260313; PMID:7741716
A;Stetus; preliminary
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     SMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDSAQLVLKK 307
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                                                              GFGGTAGMAFVGTVCSRSHAGGINVFGQ-ITVETFASIVAHELGHNLGMNHDDGRDCSCG
                                                                                                                                                                                                                                                                                                                                                                    AKSCIMNSGA---SGSRNFSSCSAEDFEKLTLNKGGNCLLNIPKPDEAYSAPS-CGNKLV
                                                                                                                                                                                                                DLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECY
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                                          EKSNYVGATFQGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCS
                                                                                                                                                                                          BAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMCRPSFEEC
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JC7850
disintegrin and metalloproteinase(ADAM) 9 protein, short form - human
N;Alternate names: MCC9 protein; meltrin gamma
C;Species: Homo sapiens (man)
C;Accession: JC7850
R;Hotoda, N.; Koike, H.; Sasagawa, N.; Ishiura, S.
Biochem. Biophys. Res. Commun. 293, 800-805, 2002
A;Title: A secreted form of human ADAM9 has an alpha-secretase activity for APP.
A;Reference number: JC7850
A;Molecule type: mRNA
A;Residues: J-655 AHOT>
A;Cross-references: UNIPROT:QBNFM6; GB:AF495383
C;Comment: This protein, which is a member of the a disintegrin and metalloprotease (ADA)
Lular functions. It is proteolytically active, and has an alpha-secretase activity for a
                                                                                                                437
                                                                                                                                                                                                                                                                                                                                              616
                                                                                                                                                                                       MSKERMCR PSFEECDL PEY CNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTD 497
                                                                                                                                                                                                            TPGKEVEFGPSECYSHLNSKTDVSGNCGI-SDSGYTQCEADNLQCGKLICKYVGKFLLQI 556
                                                                                                                                                                                                                                                                                                                                                            TDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGN--FPPVAIPARLPERRY 674
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                                                                                                                                                                                                                                                                                                    TrGTEMEMGSVDCFEQINTKNDITGNCGILSPGNYKACGASNWKCGKLICSYDKSEILRN 177
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                                                                                                                                      557 PRATIIYANISGHLCIAVEFASDHADSQKWNIKDGTSCGSNKVCRNQRCVSSSYLGYDCT
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     predicted
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                                                                           12;
                                          Length 357;
   (covalent) #status
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                                                                           Indels
                                    site: carbohydrate (Asn)
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A; Experimental source: myeloma cells
R; McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,
Biochem. Biophyer. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM),
A;Reference number: PC4263; MUID:97168971; PMID:9016778
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F;574-598/Region: epidermal growth factor-like
F;574-598/Region: epidermal growth factor-like
F;622-642/Domain: transmembrane #status predicted <TMI>
F;57,229,233,239/Binding site: zinc, catalytic (Cys, His, His, His, His) (inhibited) #status
F;229,233,239/Binding site: zinc, catalytic (His) (active) #status predicted
F;230/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metalloproteinase 12 (EC 3.4.24.-) precursor - human N.Alternate names: disintegrin 12; myeloma cell metalloproteinase MCMP C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Cpate: 19.Mar-1998 #text_change 09-Jul-2004 C;Accession: S71949; PC4264 R;MCKie, N.; Dallas, D.J.; Edwards, T.; Apperley, J.F.; Russell, R.G.G.; Croucher, P.I. Biochem. J. 318, 459-462, 1996 A;Title: Cloning of a novel membrane-linked metalloproteinase from human myeloma cells. A;Reference number: S71949; MUID:96404892; PMID:8809033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A) Status: nucleic acid sequence not shown; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 LAVILAQLESLSMGITYDDINKCQC-SGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFISK 364
                                                                                                                                                                            424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 GGQCKNPDNQCVNIYGYPARSAPEDCYISMNTRGDRFGNCGHPTEDQQTYVTCSDDNVFC
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                                                                                                                                                                                                                                                                                                                                                                                                 369 FAALMVHELGHNLGIQHDH-SACFCREKHFCLMHENITKESG---FSNCSSDYFHQFLRE
                                                                                                                                                                            QKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGS
                                                                                                                                                                                                                                                                                                                                               NCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKLICKYVGKFLLQIPRA----TIIYANISGHLCIAVEF--ASDHADSQKWWIKDGTSCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          596 SNKVCRNQRCVSSSYLGYDCTTDK-CNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCG---ISDSGYTQCEADNLQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710 FORKKWRT-----EDYSSDEQPESE
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A; Residues: 1-660 <MCK>
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A,Redidues: 1-905 <PER>
A,Cross-references: UNPROT:Q28476; EMBL:X79808; NID:9794072; PIDN:CAA56203.1; PID:g7940
A;Cross-references: UNPROT:Q28476; EMBL:X79808; NID:9794072; PIDN:CAA56203.1; PID:g7940
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;442-522/Domain: disintegrin homology <PIS>
F;376/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fertilin alpha-I - crab-eating macaque (Special macaque) (Crab-eating macaque) (Crabectes: Macaca fascicularis (crab-eating macaque) (Crabectes: 23-Aug-1995) #sectoriaris (crab-eating macaque) (Crabectes: 23-Aug-1995) #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 (Cracession: S5059) #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 #sequence_revision 1995 #sequence_revision 1995 #sequence_revision 1995 #sequence_revision mumber: S5059; MulD:95260313; PMID:7741716 #sequence_revision 1995 #s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCTDYSCVHHSILLYDCRPEESCHGKGVCNNLRHCHCGSGFAPPDCKNPGN---GGSVDS 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ICKYVGKFLLQIPRA----TIIYANISGHLCIAVEF--ASDHADSQKMWIKDGTSCGSNK 598
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                                                                                                                                                                                                                                                                                                                                                                                                          CMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCG---ISDSGYTQCEADNLQCGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703 AIMV----KVNFQRKKWRTEDYSSDEQPESE 729
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fertiin alpha precursor - mouse (fragment)
(Species: Mus musculus (house mouse)
(Cjace: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
(Cjacession: 149281
(Rjwolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.
(Ajacession: 169, 378-383, 1995
(Ajacesince number: 148100; MUID:95269891; PMID:7750654
                                                                                                   106 MVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVIYQVKHKKADVSL-----YNEKDIE 158
                                                                                                                             248 KFYRPLNIRIVLVGVEVWNDIDKCSISQDPFTRLHEFLDWRKIKLLPRKSHDNAQLI--- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                            QAFGGRK-CGNGYVEEGEECDCGEPEECT---NRCCNATTCTLKPDAVCAHGQCCEDCQL 473
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KIVIEGKPYTVNL-MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVV
                                DDINK-CQCSGAV----CIMNPEAIHFSGVKIFSNCSFEDFAHFISKQKSQCLHNQPRLD
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                                                                                                                                                                                                                                                                                                         213 AIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRW-KTSYLVLRPHDVAFLLVYR
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A/Molecule type: mRNA
A;Residues: 1-600 (RES.)
A;Cross-references: EMBL:U22056; NID:g965009; PIDN:AAA74920.1; PID:g965010
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82; Mismatches 256; Indels
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llarity 31.5%; Pred. No. 1e-46;
Conservative 82; Mismatches 256
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C;Superfamily: disintegrin homology
F;246-326/Domain: disintegrin homology <D
F;180/Active site: Glu #status predicted
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C;Superfamily: mouse meltrin alpha; disintegrin homology
F;421-503/Domain: disintegrin homology <DIS>
                                                                        16;
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                                                                                                                        105 VMVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVIYQV-----KHKKADVSLYNEKDIES 159
                                                                                                                                                                                                                      R------DLSFKLQSAEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQ 206
                                                                                                                                                                                                                                                      ETAKDEEEEPPSMTQLLRRRRAVLPQ---TRYVELFIVVDKERYDMMGRNQTAVREEMIL 123
                                                                                                                                                                                                                                                                                                                              LIGITNAIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRWKTSYLVL-RPHDVA 265
                                                                                                                                                                                                                                                                                                                                                      FLLVYREKSNYVGATFOGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDDI 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 NKCOCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQAV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 RDCSCGAKSCIMNSGA---SGSRNFSSCSAEDFEKLTLNKGGNCLLNIPKPDEAYSAPS- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGNAKLEAGEECDCGTEODCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMCR 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPSECYSHLNSKTDVSGNCGISDSGYTQCE-----535
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APKDCFIEVNSKGDRFGNCGFSGNEYKKCATGLSLXFHAPFLSTMLQEAVRQTGTYLGGS 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 VCCMKSDCRIVTLVKNALCGKLQCENV----QEIPVFGIVPAIIQTPSRGTKCWGVDFQL 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ADNLQCGKLICKYVGKFLLQIPRATIIYANIS----GHLCIAVEF-- 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASDHADSQKWMIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTD-KCNDRGVCNNKKHCHCS 635
                                                                                                                                                   ::::| |||:| || || || |||||||:
LLLATVLDLRGLLHLENASYGIEPLQMSSHFEHIIYRMDDVYKEPLKCGVS---NKDIEK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                     Length
                  tch 25.5%; Score 1016.5; DB 2; Length al Similarity 34.7%; Pred. No. 7.6e-62; 216; Conservative 109; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 ASYLPPDCSVQSDLWPGGSIDSG 658
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                  Query Match
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                                          Best Loca
Matches
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A;Residues: 1-609 <ZHO>
A;Cross-references: UNIPROT:Q90282; GB:U21003; NID:g710353; PIDN:AAC59672.1; PID:g710354
C;Superfamily: mouse meltrin alpha; disintegrin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catrocollastatin precursor - western diamondback rattlesnake
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 05-0ec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: S55270
R;Zhou, Q; Smith, J.B.; Grossman, M.H.
Biochem, J. 307, 411-417, 1995
A;Title: Molecular cloning and expression of catrocollastatin, a snake-venom protein
A;Reference number: S55264; MUID:95251603; PMID:7733877
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114 GSAASISTCAGLRGFFRVGSTVHLIEPLDADEEGQHAMYQAKHLQQKAGTCGVKDTNLND 173
                                                                                                                                                                                                                                                                          QC----SGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 VDFIGSTVGLAKVSALCSRH--SGAVNQDHSKNSIGVASTMAHELGHNLGMSHDEDIPGC
                                                                                                                                                                                                                                                                                                              347 YCPEPREGGGCIMT-ESIGSKFPRIFSRCSKIDLESFVTKPQTGCLTNVPDVNRFV-GGP
                                                                                                                                                                                                                                                                                                                                                                             --IMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFE
                                        L---SFKLQSAEPQQDF----AKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAI
                                                                         174 LGPRALEIYRAQPRNWLIPRETRYVELYVVADSQEFQKLGS-REAVRQRVLEVVNHVDKL
                                                                                                                   215 FVSFNITIILSSLELMIDENKIATIGEANELLHTFLRWKTSYLV-LRPHDVAFLLVYREK
                                                                                                                                                                                                 274 SNYVGATF----QGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYD-DINKC
                                                                                                                                                                                                                                                                                                                                                     385 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMC
                                                                                                                                                                                                                                                                                                                                                                                                                                  445 RPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
19.1%; Score 762; DB 2;
Best Local Similarity 29.6%; Pred. No. 1.9e-44;
Matches 181; Conservative 92; Mismatches 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGVCNNKKHCHCSASYLPPDC 643
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                                          162
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                                                                                                                                                                                                                                                                                                                                                               |::||||||||:||:||
PAEDVCDLPEYCDGSTQECPANSIMQDGTQCD-RIYYCLGGWCNNPDKQCSRIYGYPARS 363
                                                                                                                                                                                                                                                                                                                                                                                                                    554
                                                                                                                                                                                                                                                                                                                                                                                                                                        364 APEECYISVNTKANRFGNCGHPTSANFRYETCSDEDVFCGKLVCTDVRYLPKVKPLHSLL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 VLOYNCEPOEMCHGNGVCNNFKHCHCDAGFAPPDCSSPGN---GGSVDSG---PVGKPAD 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYKIVIEGKPYTVNIMOKNFLPHNFRVYSYS---GIGIMKPLDQDFQNFCHYQGYIEGYP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 KSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRD 161
                                                                                                                                                                                331 SGAVCIMNPEAIHFSGVKI----FSNCSFEDFAHFISKOKSQCLHNQPRLDPFFKQQAV 385
                                                                                                                                                                                                                                                                                                                                       PSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEF 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIPRA----TIIYANISGHLCIAVEFASDHADSQKWWIKDGTSCGSNKVCRNQRCVSSS 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLGYDC-TTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPA- 667
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                                                                                                                                          140 RPGENEGOAFLRGACSGEFAAAVEAFHHEDVLL--FAALMAHELGHNLGIQHDH----- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monocyte surface antigen MS2 precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60385
R;Yoshida, S; Sercoguchi, M; Higuchi, Y; Akizuki, S; Yamamoto, S.
Int: Immunol. 2, 585-591, 1990
A;Fitle: Molecular cloning of cDNA encoding MS2 antigen, a novel cell surface A;Feference number: A60385; MUID:91197896; PMID:1982220
                                                                                                                                                                                                       --PTCTCGPKHFCLMGEKIGKDSGFSNCSSDHFLRFLHDHRGACLLDEPGRQSRMRRAAN
                                                                                                                                                                                                                                                                                    CGNGVVEDLEECDCGSDCD----SHPCCS-PTCTLKEGAQCSEGLCCYNCTFKKKGSLCR
                        AIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRWKTSYLVLR-PHDVAFLLVYR
                                                                                                                                                                                                                                                                                                                                                                                                                    GPSECYSHLNSKTDVSGNCGISDSG---YTQCEADNLQCGKLIC---KYVGKF----LL
                                                                                                     EKSNYVGATFQGKMCDANYAGGV-VLHPRTISLESLAVILAQLLSLSMGITYDDINKCQC
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-826 < vSos.
A;Cross-references: UNIPROT: QBR3D3; EMBL:X13335
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: glycoprotein; surface antigén; transmembrane
F;10-14/Domain: signal sequence #status predicted <SIG>F;402-484/Domain: disintegrin homology <DIS>F;659-683/Domain: transmembrane #status predicted <TMM>F;530/Active site: Glu #status predicted
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                                  415 IATCRFKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGH 474
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Search completed: January 10, 2005, 22:28:33 Job time : 45 secs This Page Blank (uspto)

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077780 bos taurus
Q2860 oryctolagus
Q63202 ratus morv
Q60718 mus musculu
G60411 cavia porce
Q95194 macaca fasc
Q95194 momo sapien
Q8tc27 homo sapien
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Q6uxf9 homo sapien
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Q28483 macaca fasc
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Q2289 mus musculu
Q60472 cavia porce
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Q8cdo mus musculu
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Q9640 mus musculu
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Q1443 homo sapien
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Q6p2g0 homo sapien
Aah64547 homo sapi
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1 MWVLFLLSGLGGLRMDSNFD......WRTEDYSSDEQPESESEPKG
                                                                                                                                                                   1825181
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                 1825181 segs, 575374646 residues
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Q866A8
AD02_BOVIN
AD02_RABIT
AD02_RADIS
AD02_CAVPO
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AD02_MACFA
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2: uniprot_trembl:*
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060816 AD09 MOUSE AD09 MOUSE 042595 028659 019061 028477 AD1A MOUSE AD04 RAT 028476 019060	060410
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## ALIGNMENTS

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TISSUE=Testis;
MEDLINE=97224507; PubMed=9070941;
Burkin H.R., Burkin D.J., Davey P.M., Griffin D.K., Affara N.A.;
"Mapping, sequence, and expression analysis of the human fertilin beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vidaeus C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows T.B.,
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                099955; P78326; Q9UQQ8; 30-MAX-2000 (Rel. 39, Created) 30-MAX-2000 (Rel. 39, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) ADAM 2 precursor (A disintegrin and metalloproteinase domain 2) (Fertilin beta subunit) (PH-30) (PH30).
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MEDLINE=96295488; PubMed=8702389;
MEDLINE=96295488; PubMed=8702389;
Gupta S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F.;
"Molecular cloning of the human fertilin beta subunit.";
Biochem. Blophys. Res. Commun. 224:318-326(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herr J.C.;
"Human fertilin beta: identification, characterization, and chronsonal mapping of an ADAM gene family member.";
Mol. Reprod. Dev. 46:363-369(1997).
    735 AA
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Testis; PubMed=9041139; MEDLINE=97193554; PubMed=9041139; Gr
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Homo sapiens (Human).
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Genomics 40:190-192(1997).
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Name=2;
IsoId=099956-2; Sequence=VSP 005471;
Note=2:
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B., Schmitz J., Myers R.M., Schein J.B., Schalska U., Skalska U., Skalska U., Scherth A., Schein J.B., Ones S.J.M., Marra M.A., Schein J.B., Ones S.J.M., Marra M.A., Human M. Initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                            Min; 90153; ...

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005178; F:integrin binding; TAS.

R GO; GO:0008237; F:metallopeptidase activity; TAS.

R GO; GO:0007342; P:fusion of sperm to egg plasma membrane; TAS.

R InterPro; IPR006586; ADAM cysteine.

R InterPro; IPR001762; Disintegrin.

R InterPro; IPR001590; Peptidase M12B.

R Pfam; PF00200; Disintegrin; 1.

R Pfam; PF01562; Pep M12B propep; 1.

R Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q99965-1; Sequence=Displayed;
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EMBL; AJ133005; CAB40813.1; --
EMBL; BC034997; AAH34957.1; --
PIR; JC4861; JC4861.
MSSP; B30403; INAY.
MENOPS; M12.950; --
Genew; HGNC:198; ADAM2.
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                             Probom; PD000664; Disintegrin; 1.
SMART; SM00669; ACK; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS50121; ADAM MEPRO; 1.
PROSITE; PS50121; DISINTEGRIN 1; 1.
PROSITE; PS00022; BGF 1; FALSE NEG.
PROSITE; PS01086; EGF 2; FALSE NEG.
PROSITE; PS01186; EGF 2; FALSE NEG.
Alternative splicing; Cell adhesion; EGF-like domain; Glycoprotein;
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Extracellular (Potential)
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Metalloprotease-like.
Disintegrin-like.
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D -> H (in Ref. 3)
V -> G (in Ref. 3)
V -> G (in Ref. 3)
V -> A (in Ref. 2)
I -> T (in Ref. 1)
I -> T (in Ref. 1)
G -> S (in Ref. 1)
G -> S (in Ref. 3)
G -> C (in Ref. 3)
G -> C (in Ref. 3)
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PRINTS; PR00289; DISINTEGRIN
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Best Local Similarity 99.7
Matches 733; Conservative
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SIGNAL 1 16
PROPEP 17 174
CHAIN 175 735
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                                                                                                           HFISKOKSQCLHNOPRLDFFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR 420
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                                                                               TISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFA 359
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MEDLINE-96341733; PubMed=8720115;

Ramaraco C.S., Myles D.G., White J.M., Primakoff P.;

Ramaraco C.S., Myles D.G., White J.M., Primakoff P.;

Initial evaluation of fertilin as an immunocontraceptive antigen and molecular cloning of the cynomolgus monkey fertilin beta subunit.";

Mol. Reprod. Dev. 43:70-75(1996).

-!- FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By
                                                                                                                                                                                                                                                                                                                                                                                                             QWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL
                                                                                                                                                                                                                                                                                                    FKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLN
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MEDLINE=95260313; PubMed=7741716;
Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
"Cloning and analysis of monkey fertilin reveals novel alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
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                                                                                                                                                                                                       ENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSIEPQKDFAKYI 180
                                                                                                                                                                                                                                                      EMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLINAIFVSFNITIILSSLELWIDENKIATT 239
                                                                                                                                                                                                                                                                                                                                                TISLESLAVILAQLISLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGN 659
                                                                                                                                                                                                                                                                                                                             GEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPR 299
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                                                                                                                                                                                  ENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYI
                                                                                                                                                                                                                                                                             QWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL
                                                                                                           MOKNFLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR
                                     MW-VLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNL
   Gaps
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Catarrhini; Hominidae; Homo.
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 32; Indels
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Last annotation update)
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Mammalia; Eutheria; Primates;
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05-JUL-2004 (TrEMBLrel. 27,
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ADAMZ protein.
 672; Conservative
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;

" "Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences."
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InterPro; DFR00586; ADAM_cysteine.
InterPro; DFR001762; Dishifteginh.
InterPro; DFR001762; Dishifteginh.
InterPro; DRR001590; Peptidase M12B.
InterPro; DRR002870; Peptidase M12B.
Pfam; PF002009; Dishitteginh; 1.
Pfam; PF01562; Pep M12B_propep; 1.
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SWART; SM00669; ACR; 1.
SMART; SM0050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
SEQUENCE 579 AA, 64795 MW; 1F7AFO
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ProDom; PD000664; Disintegrin; 1.
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Altacher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Haich F.,
A Bapleton M., Soarse M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.B.,
A Brownstein M.J., Usdin T.B., Toonhyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Usdin T.B., Toonhyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Widnar T.B., Toonhyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Wakenan R.J., Makenan R.D., Mullahy S.J.,
A Boak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
A Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A., Sodergren E.J., Lu X., Gibbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
A Dones S.J., Marra M.A.,
A mouse CNNX semience "... Smailus D.E., Schnerch A., Schein J.E.,
And mouse CNNX semiences "...
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445 CRNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCKSASYLPPDCSVQSDLWPGGSIDSGN
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                                          QWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL
                                                                                             540 QCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKWMIKDGTSCGSNKV
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                                                                                                                                                CRNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGN
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Catarrhini, Hominidae, Homo.
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EMBL; BC064547; AAH64547.1; -.
SEQUENCE 579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ADAM2 protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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les 577; Conservative
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1 MW-VLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNL 59

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MOKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF
                                                                                                                                                                                61 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Day A.E., Quilter C.R., Sargent C.A., Mileham A.J.;
Chromosomal mapping, sequence and transcription analysis of the portine fertilin beta gene (ADAM2).";
Anim. Genet. 34:375-378(2003).
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NCBI_TaxID=9913;
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                                   Thesis (2004), Department of Applied Sciences, Anglia Polytechnic University, Cambridge, United Kingdom.
EMBL: AJ309003; CAC84225.2; -. HSSP; P18619; 1FVL.
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                                                                                                                                                                                                                                                                                                                                 tch 70.8%; Score 2820; DB 2; Length 735; al Similarity 68.6%; Pred. No. 2.1e-183; 502; Conservative 96; Mismatches 132; Indels 2
                                                                           MEMORS; MLZ.950; —.

GO; GO:000422; F:metalloendopeptidase activity; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:00003676; F:nucleic acid binding; IEA.

InterPro; IRR00686; ADAM cysteine.

InterPro; IRR000742; EGF 2.

InterPro; IRR000742; EGF 2.

InterPro; IRR000894; Nucleic acid OB.

InterPro; IRR001500; Peptidase MIZB.

InterPro; IRR001600; Disintegrin; 1.

RANNT; SN00068; ACR; 1.

SWART; SN00068; ACR; 1.
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PROSITE; PSS0215; ADAM MEPRO; 1.
PROSITE; PSS0427; DISINTEGRIN 1; 1
PROSITE; PSS0214; DISINTEGRIN 2; 1.
PROSITE; PSS026; EGF 3; 1. 1
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[2]
SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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602
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1. SUBUNIT: Heterodimer with ADAMI/fertilin alpha.
1. SUBCELDULAR LOCATION: Type I membrane protein.
1. TASUES PERCIFICITY: Expressed specifically in testis.
1. TASUE SPECIFICITY: Expressed specifically in testis.
1. DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain could be involved in the binding (by similarity).
1. PTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
1. SIMILARITY: Concains I disintegrin domain.
1. SIMILARITY: Contains I EGF-like domain.
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-1- FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
KLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKVCRN
                                       603 QRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPP
                                                                                                                                                                                      663 VAIP-ARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waters S.I., White J.M.; "Biochemical and molecular characterization of bovine fertilin alpha and beta (ADAM 1 and ADAM 2): a candidate sperm-egg binding/fusion
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
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InterPro; IPR006586; ADAM_cysteine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ADAM2; Synonyms=FTNB;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDEOPESESEPK 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           723 SDEQLESESETK 734
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                              GSACDTGLCCESCAFIPKGHICRGSTDECDLHEYCNGSSAACQEDVYVQDGHPCGQNQWL 482
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-:- SUBCELULAR LOCATION: Type I membrane protein.
-:- SUBCELULAR LOCATION: Type I membrane protein.
-:- DOMAIN: A tripeptide motif (VGE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding we similarity).
-:- PTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
-:- SIMILARITY: Concains I disintegrin domain.
-:- SIMILARITY: Contains I EGF-like domain.
                         SKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKA
                                                                                                                                                                                                      CIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG
                                                                                                                                                                                                                              MEDLINE=97071141; PubMed=8914066;
MEDLINE=97071141; PubMed=8914066;
METATION: C.N., Holland M.K.;
"Cloning and expression of recombinant rabbit fertilin.";
MOI. Reprod. Dev. 45:107-116(1996).
-1-FUNCTION: Sperm surface membrane protein that may be involved in apperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disnitegrin and metalloproteinase domain 2)
(Fertilin beta subunit) (PH-30) (PH30 (PH30-beta).
(Name-ADAM2; Synonyms=FTNB;
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Metalloprotease-like.
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Pred. No. 8.4e-177;
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Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR01289; DISINTEGRIN; 1.
PRODOM; PD000664; Disintegrin; 1.
SMART; SM00669; ACR; 1.
SMART; SM00060; DISIN; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00427; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS00124; DISINTEGRIN 1; 1.
PROSITE; PS00124; DISINTEGRIN 1; 1.
PROSITE; PS00126; EGF 1; FALSE NEG.
PROSITE; PS01186; EGF 2; PALSE NEG.
PROSITE; PS01186; EGF 3; 7.
Cell adhesion; EGF-like domain; Glycog
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                InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF InterPro; IPR006994; Wouleic acid OB InterPro; IPR001590; Peptidase MIZB.
InterPro; IPR002870; Peptidase MIZB.
Disintegrin
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STRAINE-Sprague-Dawley; TISSUE-Testis;

MEDLINE-Sprague-Dawley; TISSUE-Testis;

MEDLINE-Sprague-Dawley; TISSUE-Testis;

MCLaudhiln B.A., Frayne J., Barker H.L., Jury J.A., Jones R.,

MCLaudhiln B.A., Frayne J., Barker H.L., Jury J.A., Jones R.,

MCLaudhiln B.A., Frayne J., Barker H.L., Jury J.A., Jones R.,

T "Cloning and sequence analysis of rat fertilin alpha and beta -
developmental expression, processing and immunolocalization.";

MOI. Hum. Reprod. 3:801-80(1997).

C -!- FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during

fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
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                                                                                                                                                                       LESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFI 362
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   VIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKIATTGEA
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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063202;
28-FEB-2003 (Rel. 41, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain (Fertilin beta subunit) (FH-30) (FH30) (FH30-beta).
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Rattus norvegicus (Rat).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                               InterPro; IRR006586; ADAM_cysteine.

BR InterPro; IPR000742; EGF 2.

BR InterPro; IPR000742; EGF 2.

BR InterPro; IPR000742; EGF 2.

BR InterPro; IPR0008299; Nucleic acid OB.

BR InterPro; IPR0008994; Nucleic acid OB.

BR InterPro; IPR0008994; Nucleic acid OB.

BR InterPro; IPR001890; Peptidase_M12B.

BR InterPro; IPR001890; Interprin; 1.

BROSITE; PS00180; BGF 1; FALSE_NEG.

BR ROSITE; PS00186; EGF 2; FALSE_NEG.

BR PROSITE; PS00186; EGF 3; 1.

BROSITE; PS00186; EGF 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VLFLLCGLSGLRTKENSERLHVQVTVPEKMRSVTSEGFETEVVYNIVIEGKTYTLNLMQK
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llarity 64.4%; Pred. No. 3.3e-174;
Conservative 106; Mismatches 142; Indels 10
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Cys-rich.
EgF-like.
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                                                                                                                                                         EMBL; U46070; AAA93321.1; -. HSSP; P30403; 1N4Y.
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301 VALHPKAVTLESLAIILVQLLSLSMGVAYDDVNTCQCGVPICVMNPEALHSSGVRSFSNC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 RGVLQFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQ
                                                                                                                                                                                                                                                                                                                                                             SMEDFSKFIVSQSSHCLQNQPHLQPSYK-MAVCGNGELEEGEVCDCG-QEGCDDKPPPCC
                                            61 TYILNLWQKAFLPPNFRVYSYDSTGIMRPLEQKEQNICYFQGYIEGYPNSMVIVSTCTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                599 VCGSGKVCLNQECVEDIFLNYDCTPEKCNHHGVCNNKKHCHCEPTYLPPDCKNTEDTWPG
           1 MWVLFL----LSGLGGL----RMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGK
                                                                                                                 54 PYTVNIMQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGL
                                                                                                                                                                                                                                                                                                                              DPAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITILLSSLELWIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                       NKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFEDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPG
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TISSUE=Testis;
MEDLINE=96019260; PubMed=7593287;
Evans J.P., Schultz R.M., Kopf G.S.;
"Mouse sperm-egg plasma membrane interactions: analysis of roles of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AD02 MOUSE STANDARD, PRT, 735 AA.

Q60718; Q60814; Q9D4G3; Q9QWJ0;
28-FEB-2003 (Rel. 41, Lest sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
ADAM 2 precursor (A disincegrin and metalloproteinase domain (Fertilin beta subunit) (FH-30) (FH30) (FH30-beta).

Name=Adam2; Synonyms=Ftnb, Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: A tripeptide motif (NQE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).

PTM: The prodomain and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Glycoprotein; Signal; Transmembrane.
Potential.
By similarity.
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Extracellular (Potential)
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By similarity.
Potential.
By similarity.
By similarity.
By similarity.
N-linked (GlONAC...) (CONTRIBLE (GLONAC...) (CONTRI
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Cytoplasmic (Potential)
Metalloprotease-like.
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                                                                                                                                                                                    SIMILARITY: Belongs to peptidase family M12B. SIMILARITY: Contains 1 disintegrin domain. SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.2%; Score 2479.5; DB 1;
ilarity 59.6%; Pred. No. 3.1e-160;
Conservative 116; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GlcNAc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGENIN 1; FALSE_NEG.
PROSITE; PS00121; DISINTEGENIN 2; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
Cell adhesion; EGF_1ike domain; Glycoprotesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGD; 69299; Adam2.
InterPro; IPR00686; ADAM cysteine.
InterPro; IPR001762; Dishittegrin.
InterPro; IPR001762; Dishittegrin.
InterPro; IPR006209; EGF_1ike.
InterPro; IPR006210; EGF_1ike.
InterPro; IPR008994; Nucleic_acid OB.
InterPro; IPR001890; Peptidase_M12B.
InterPro; IPR002870; Peptidase_M12B.
InterPro; IPR002870; Peptidase_M12B.
Pfam; PF01562; Pep_M12B_propep; I.
Pfam; PF01421; Repro]yslin; I.
ProDom; PD000664; Disintegrin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cys-rich.
EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X99794; CAA68127.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82310 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000664; Disinteg
SMART; SM00608; ACR; 1.
SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P18619; 1FVL.
MEROPS; M12.950; -.
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737 AA;
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Matches 442; (
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ProDom; PD000664; Disintegrin; 1.
SWART; SW00608; ACR; 1.
SWART; SW00050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 1; FALSE_NEG.
PROSITE; PS0012; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; FALSE_NEG.
PROSITE; PS50026; EGF 2; FALSE_NEG.
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity. ADAM 2.
                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                          Interpro; IPR000742; EGF 2.
Interpro; IPR006209; EGF 1ike.
Interpro; IPR006309; Nucleic_acid_OB.
Interpro; IPR001590; Peptidase M12B.
Interpro; IPR002870; Peptidase_M12B.
Pfam; PF00200; Disintegrin, 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                   InterPro; IPR006586; ADAM_cysteine.
InterPro; IPR001762; Disintegrin.
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82374 MW;
                                                                                                         EMBL; U16242; AAA90980.1; -.. EMBL; U38806; AAD04207.1; -.. EMBL; AK01655; BAB30298.1; -.. EMBL; U22057; AAA74921.1; -.. HSSP; P17347; ZECH.
                                                                                                                                                                                                                          MEROPS; M12.950; -.
MGD; MGI:1340894; Adam2.
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712
735 AA;
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    TRAIN-CE-YBL/60; TISSUE=Teetis;

XR SEQUENCE FYON N.A.

SEQUENCE FYON N.A.

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

AN OKAZARI Y., Furuno M., Kaaukawa T., Adachi J., Bornoh H., Krondo S.,

AN Adachi I., Osatco N., Saitco R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Balla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,

Andasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Warckawa N., Jackson I.J., Jarvis B.D.,

Anglott D.R., Maltais L., Marchonni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Numata K., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Raid J., Ring B.Z., Ringwald M.,

Sultana R., Takenaka Y., Taylor M.S., Tesadale R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Walls C.,

Milming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Milming L.G., Walki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Allara A., Hashizume W., Imotani K., Ishingawa A.,

Milming M., Sakai K., Sasaki K., Sasaki K., Shinagawa A.,

Marazaki A., Sakai K., Sasaki K., Shasaki D., Shibata K., Shinagawa A.,

Malara A., Hashizume W., Imotani K., Itaha K., Shinagawa A.,

Malara A., Hashishizume W., Imotani K., Inder E.S., Rogers J.,

Myazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malayazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malayazaki A., Sakai K., Sasaki D., Shibata K., Shorton M., Shinaga K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Heterodimer with ADAMI/fertilin alpha.
SUBUNIT: Heterodimer with ADAMI/fertilin alpha.
SUBCELLUJAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed specifically in testis.
DOMAIN: A tripoptide motif (QDB) within disintegrin-like domain could be involved in the binding for egg integrin receptor and thus could mediate sperim/egg binding fly similarity).
PTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa.
SIMILARITY: Contains 1 disintegrin domain.
SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95269891; PubMed=7750654; Wolfsberg T.G., Straight P.D., Gerena R.L., Huovila A.-P., Primakoff P., Myles D.G., White J.M., AppM, a widely distributed and developmentally regulated gene family encoding membrane proteins with a disintegrin and metalloprotease
  egg integrins and the mouse sperm homologue of PH-30 (fertilin)
                                                                                  SEQUENCE FROM N.A. Gupta S.K., Palladino L.O., Mark G.E., Hollis G.F.; Submitted.(OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                         Cell Sci. 108:3267-3278(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 17-735 FROM N.A.
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                                                                                                                                                                              SEQUENCE FROM N.A.
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
SIGNAL 1 18 Potential
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TG -> QA (in Ref. 4).
A -> L (in Ref. 4).
DV -> RR. (in Ref. 4).
R -> T (in Ref. 4).
S -> T (in Ref. 4).
A -> R (in Ref. 4).
A -> R (in Ref. 1).
Q -> P (in Ref. 1).
WF 75EC8529CF588E2B CRC64;
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(Potential).
(Potential).
(Potential).
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Cytoplasmic (Potential).
Metalloprotease-like.
Disintegrin-like.
Cya-rich.
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LSOS -> IRHE (in Ref. 4)
GT -> A (in Ref. 4).
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SIGNAL
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                                                                                                                                                                                                                                            DFAKYIEMHVIVEKQLYNHMGSDTTVVAQKVPQLIGLTNAIFVSFNITIILSSLELWIDE 233
                                                                                                                                                                                                                                                                                                                                   VVLHPRIISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNC 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGSNKVCRNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGG 653
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                                                    1 MWLILLLISGLSELGGLSQSQTEGTREKLHVQVTVPEKIRSVTSNGYETQVTYNLKIEGK 60
                                                                                                                                                                                                                                                                                                                 NKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGG
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                                  1 MW-VLFLLSG---LGGL---RMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGK
 Gaps
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Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain (Fertilin beta subunit) (PH-30) (PH30).
442; Conservative 119; Mismatches 166; Indels
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KWRMDDFSSEEQFESESESK 734
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TISSUE=Testis;
MEDLINE=94068486; PubMed=8248170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Heterodimer with ADAMI/fertilin alpha.
-!- SUBCELDULAR LOCATION: Type I membrane protein.
-!- SUBCELDULAR LOCATION: Type I membrane protein.
-!- TASUES SECTIFICITY: Expressed specifically in testis.
-!- DEVELOPMENTAL STAGE: Expressed specifically in testis.
-!- DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).
-!- FTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatoza (By similarity).
-!- SIMILARITY: Contains I EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A potential fusion peptide and an integrin ligand domain in a protein active in sperm-egg fusion.";
Nature 356:248-252(1992).
                                                                      "The precursor region of a protein active in sperm-egg fusion contains a metalloprotease and a disintegrin domain: structural, functional,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrine receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000664; Disintegrin; 1.
SWART; SW00669; ACR; 1.
SWART; SW00050; DISIN; 1.
SWART; SW00050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50215; DISINTEGRIN 1; 1.
PROSITE; PS00022; EGF 1; FALSE NEG.
PROSITE; PS01186; EGF 2; FALSE NEG.
PROSITE; PS01086; EGF 2; FALSE NEG.
PROSITE; PS01086; EGF 2; FALSE NEG.
CG11 adhesion; EGF-1iKe domain; Glycoprotein; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                            Blobel C.P., Wolfsberg T.G., Turck C.W., Myles D.G., Primakoff P., White J.M.;
Wolfsberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
By similarity.
ADAM 2.
Extracellular (Potential).
                                                                                                                                                and evolutionary implications.";
Proc. Natl. Acad. Sci. U.S.A. 90:10783-10787(1993)
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InterPro; INT.0906586; ADAM cysteine.
InterPro; IPR000762; Disintegrin.
InterPro; IPR000742; EGF 2.
InterPro; IPR000509; EGF 1ike.
InterPro; IPR000509; EGF 1ike.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR001590; Peptidase M12B.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92204234; PubMed=1552944;
                                                                                                                                                                                                                                                                        SEQUENCE OF 383-735 FROM N.A.
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OKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKIATTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                           58.4%; Score 2326; DB 1; Length 735;
llarity 56.1%; Pred. No. 8.8e-150;
Conservative 125; Mismatches 182; Indels 16
                     Cytoplasmic (Potential).
Metalloprotease-like.
Disintegrin-like.
Cys-rich.
EGF-like.
By similarity.
By similarity.
Potential.
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By similarity.
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735 AA;
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RESULT 11 AD18\_MACFA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).

--- PTM: The prodomain and the metalloprotease-like domain are cleaved during the epididymal maturation of the spermatozoa.

--- SIMILARITY: Belongs to peptidase family M12B.

--- SIMILARITY: Contains 1 GGF-like domain.
                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-007-2004 (Rel. 45, Last annotation update)
ADAM 19 precursor (A disintegrin and metalloproteinase domain 18)
(Transmembrane metalloproteinase-like, disintegrin-like, and cysteinerich protein III) (tMDC III).
Name-ADAM18; Synonyms-TMDC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000664, Disintegrin; 1, SMART; SM00050; ACR; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN 2; PROSITE; PS00022; EGF 1; FALSE NEG.
PROSITE; PS00022; EGF 1; FALSE NEG.
PROSITE; PS00022; EGF 1; FALSE NEG.
PROSITE; PS00026; EGF 3; 1.
PROSITE; PS00026; EGF 3; 1.
EGF-1ike domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                   may be involved in
                                                                                                                                                                                                                                                                                                                                      Frayne J., Jury J.A., Barker H.L., Perry A.C.F., Jones R., Hall L., "Macaque MDC family of proteins: sequence analysis, tissue distribution and processing in the male reproductive tract."; Mol. Hum. Reprod. 4:429-437(1998).

-I- FUNCTION: Sperm surface membrane protein that may be involved in spermatogenesis and fertilization. This is a non catalytic metalloprotease-like protein (By similarity).

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: Expressed predominantly in adult and
                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular (Potential) Potential. Cytoplasmic (Potential).
746 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006586; ADAM_cysteine.
InterPro; IPR001762; Disintegrin.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 11ke.
InterPro; IPR001590; Peptidase_M12B.
InterPro; IPR001590; Peptidase_M12B.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF01421; Reprojysin; 1.
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STANDARD;
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NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLPQNFLVYTYNBAGSLHSESPYFMHCHYQGYAAEFPNSFVTLSICSGLRGFLQFEN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POYLEIYIIVEKALYDYMGSEMMAVTQKIVQVIGLVNTMFTQFRLTVTLSSLELWSNENQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDI 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGTMCGPEMYCVNKTCRKVHLTGYNCNTTTKCKGKGICNNFGNCQCPPGHKPPDCKFQFG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSYGIEPLESSVGFEHVIYQVKHKKADVSLY--NEKDIESRDLSFKLQSAEPQQDFAK-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --YIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSF 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCRFXAGSNCAEGPCC-ENCLFMSKERMCRPSFE-ECDLPEYCNGSSASCPENHYVQTG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEADNLQCGKLICKYVGKFLLQIPRATIIYANISGHLCIAV----EFASDHADSQKMWIK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPMRW---PFFLFIPFFIIFCVLIAIM 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFEN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 FLIALLIFELGRIQAHVGSEGIFLHVIVPRKILSNDSEVSERKMIYIITIDGGPYTLHIRK 62
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Metalloprotease-like.
Disintegrin-like
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C.-I. FUNCTIONS: Sperm surface membrane procedun that may be involved in spermatogenesis and fertilization. This is a non catalytic metalloprotease-like protein (By similarity).

C.-I. SUBCELLULAR LOCATION: Type I membrane protein.

C.-I. SUBCELLULAR LOCATION: Type I membrane protein.

C.-I. DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain.

C.-I. DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain.

C.-I. PIM: The prodomain and the metalloprotease-like domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).

C.-I. SIMILARITY: Contains I disintegrin domain.

C.-I. SIMILARITY: Contains I EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch/o.ch).
                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-CCT-2004 (Rel. 45, Last annotation update)
ADAM 18 precursor (A disintegrin and metalloproteinase domain 18)
(Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-
rich protein III) (EMDC III)
Name-ADAMI8; Synonyms-TMDC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall L., Frayne J., Dimsey E.A.; "Nucleotide sequence of the human tMDC III sperm surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0002237; F:metallopeptidae activity; TAS.
GO; GO:0007283; P:spermatogenesis; TAS.
InterPro; IPR001586; ADAM_Cysteine.
InterPro; IPR001586; ADAM_Cysteine.
InterPro; IPR001590; BGF like.
InterPro; IPR001590; Peptidase_M12B.
InterPro; IPR002809; Peptidase_M12B.
                                                                                                                                                                                                                                                      739 AA.
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SMART; SMO0609; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50217; DISINTEGRIN 1; FALSE_NEG.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
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Pfam; PF01562; Pep M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
Probom; PD000664; Disintegrin; 1.
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HSSP; P83469; 1MPZ.
                                          |:| : |
----FKRNEIR 714
                                                                                                                                                                                                                                                              STANDARD;
VKVNFQRKKWR
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                                                                                                                                                                                                                    AD18_HUMAN
ID AD18_HUMAN
                                                                     708
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MEDLINE=22388257; PubMed=12477932;

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschuls S.P., Zeoberg B. B., Buetow K.H., Schaefer C.P., Bhat N.K.,

Altschul S.F., Zeoberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altschul S.F., Zoarea H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raba S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullah S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Marsa M.A.; Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human

Mines S.J., Marra M.A.;

and mouse C.NA sequences.",
650 WPGGSIDSGNPPPVALPARLPERRYIENIYHSKPMRW---PFFLFIPPFIIFCVLIAIMV 706
                                                                                     GTSCGSNKVCRNORCVSSSYLGYDC-TTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDL
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Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush
                                                                                                                                                                                                                                                                                                                                                                                                             1-JUN-2002 (TrEMBLrel. 21, Created)
1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
1-OCT-2004 (TrEMBLrel. 28, Last annotation update)
disintegrin and metalloprotease domain 32 (Similar to MDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                          787 AA.
                                                                                                                                                                                                                              KVNFQRKKWRTE--DYSSDEQPESESEPKG 734
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=ADAM32; ORFNames=UNQ5982;
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Submitted (JUL-2002)
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Submitted (MAY-2002)
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SEQUENCE FROM N.A.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFPNSFVTLSICSGLRGFLQFENI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYGIEPLESSVGFEHVIYQVKHKKADVSL--YNEKDIESRDLSFKLQSAEPQQDFAK--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 ATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVVL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFAHFISKOKSOCLHNOPRLDPFFKOOAVCGNAKLEAGEECDCGTEQDCALIGETCCDIA 416
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DYRYFVSKFETKCLQKLSNLQPLHQNQPVCGNGILESNEECDCGNKNECQF--KKCCDYN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCRFKAGSNCAEGPCC-ENCLFMSKERMCRPSFE-ECDLPEYCNGSSASCPENHYVQTGH 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCKLGTAYCYNGQCQTTDNQCAKIFGKGAQGAPFACFKEVNSLHERSENCGFKNSQPLPC 541
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                                                                                                      Extracellular (Potential)
                                                                                                                                           Cytoplasmic (Potential)
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39.7%; Score 13.6e-99;
Best Local Similarity 41.9%; Pred. No. 3.6e-99;
Matches 314; Conservative 128; Mismatches 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CNAC.
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By similarity.
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N-linked (GlCN)
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EGF 2; FALSE NEG
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625
739 AA;
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57 VNLMQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV 116
                                                                                                               538 KYVECGWRNLICGRLVCTYPTRKPFHQENGDVIYAFVRDSVCITVDYKLPRTVPDPLAVK 597
                                                                                                                                                                             174 D--FAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWI 231
                                                                                                                                                                                                                        SDLWPGGSI----DSGNFPPVAIPARLPERRYIENIYHSKPMRW--PFFLFFFIFFCV 700
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                                                                                              530 GYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIK
                                QTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS
                                                                                                                                                           DGTSCGSNKVCRNQRCVSSSYL---GYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MWVLFLLSGLGGLRMD-SNFDSLPVQITVPEKIRSIIKEGIE---SQASYKIVIEGKPYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: Bioinformatics Assessment.", Genome Res. 13:226-2270 (2003). EMBL, AY358739; AAQ890991: -. SEQUENCE 787 AA, 87933 MW; 3D84CACFECCIA12E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pubmed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chark H.F., Gurney A.L., Abaya E., Caurell B., Deuel B., Dowd J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd J. Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis D., Kim H.S., Klimowski L., Johnson S., Lees J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
38.3%; Score 1524.5; DB 2; Length 787;
Best Local Similarity 41.1%; Pred. No. 3.4e-95;
Matches 310; Conservative 134; Mismatches 259; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Butheria, Primata, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                    LIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG
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GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001762; Disintegrin.
InterPro; IPR006209; EGF like.
InterPro; IPR006299; EGF like.
InterPro; IPR006299; Peptidase_MI2B.
InterPro; IPR002870; Peptidase_MI2B.
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Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
Proposite; PS50115; ADAM MERRO; 1.
PROSITE; PS50115; DISINTEGRIN; 1.
PROSITE; PS50115; DISINTEGRIN 2; 1.
PROSITE; PS50126; EGF 2; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 1.
Integrin; Metalloprotease; Protease.
SEQUENCE 787 AA; 87933 MW; 3D84CACFECCIA12E CRC64;
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Godowski P.;
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MEDLINE-22388257; PubMed=12477932;

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MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MISCHOL S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Habet N.K.,

MAISCHOL S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Habet N.K.,

MATCHONKO L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scheefer T.E., Scheefer T.E., Scheefer T.E.,

Brownstein M., Soaces M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makrigher A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
                                                                               181 PDLFPLYLEMHIVVDKTLYDYWGSDSMIVTNKVIEIVGLANSMFTQFKVTIVLSSLELWS 240
                                                                                                                NCSFEDFAHFISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGET 411
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                                    241 DENKISTVGEADELLOKFLEWKOSYLNLRPHDIAYLLIYMDYPRYLGAVFPGTMCITRYS
                                                                   GGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCOCSGAVCIMNPEALHFSGVKIFS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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analysis of more than 15,000 full-length human
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                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Submitted (MAR-2002) to the
EMBL; BC026085; AAH26085.1;
HSSP; P30403; 1N4Y.
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Search completed: January 10, 2005, 22:27:44 Job time : 204 secs This Page Blank (USDIO)

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January 10, 2005, 22:20:47 ; Search time 148 Seconds (without alignments) 1788.239 Million cell updates/sec
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1 MWVLFLLSGLGGLRMDSNFD......WRTEDYSSDEQPESESEPKG 734
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| Cgn2_6/ptodata/1/pubpaa/US06_WEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMALES				
Result		Query	Query						
Š.	Score	Match	Length	8	ΩI	Description			
Т	3984	100.0	•	14	US-10-054-683-19	Sequence 1	6	Appl	
7	3984	100.0	•	14	US-10-205-823-10	Sequence 1	0	Appl	
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4	3969.5	9.66	735	14	US-10-205-823-8	Sequence 8	Α,	ippli	
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9	1524.5	38.3	•	14	US-10-227-884-90	Sequence 9		Appl	
7	1524.5	38.3	•	14	US-10-230-163-90			Appl	
œ	1524.5	38.3	•	14	US-10-230-338-90			Appl	
σ	1524.5	38.3	•	14	US-10-218-631-90	Seguence 9		Appl	
10	1524.5	38.3		14	US-10-230-414-90			Appl	
11	1524.5	38.3	787	14	US-10-232-224-90		90,	Appl	
12	1524.5	38.3		14	US-10-216-159A-90	Sequence 9		Appl	
13	1524.5	38.3		14	US-10-218-849-90	Sequence 9		Appl	

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Gaps ö 61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQPE 120

1 MWYLFLLSGLGGLRMDSNFDSLPVQTTVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLM 60

1 MWVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLM 60

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Query Match 100.0%; Score 3984; DB 14; Length 734; Best Local Similarity 100.0%; Pred. No. 3.5e-311; Matches 734; Conservative 0; Mismatches 0; Indels 0;

TYPE: PRT
CRGANISM: Homo sapiens
US-10-054-683-19

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29	1524.		œ	787		-10-219-468-9	90,
30	1524.		æ	787	14	-10-219-478-9	90,
31	1524.		æ	787		-10-219-536-9	90,
32	1524.		œ	787		-10-233-205-9	90,
33	1524.		8	787		-10-219-072-9	90
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32	1524.		œ	787		-10-219-474-9	90,
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	AL INF	ORMA	TION:				
APPL	ICANT:	old	APPLICANT: Old, Lloyd	Ġ.			
	APPLICANT:	S	Scanlan, Matthew	Matth	ew J	•	
; APPL	APPLICANT:	S	en, Ya	o-Taer	<u>م</u>		•
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FILE	REFER SNT AD	ENCE	. LO46	1//125	. S.	FILE REFERENCE: LO461/7125 (JRV)	
. CORR	ENT AF	LING	DATE	2002	-10-	7.10/054,665	
PRIO	RAPPL	ICAT	ION NOI	MBER:	US 60	0/280,718	
PRIOR		NG	FILING DATE: 2001-03-30	001-03	1-30		
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, PRIOR		NG	FILING DATE: 2001-04		-20		
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100.0%; Score 3984;
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 734; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR PLING DATE: 2001-03-15
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.00
LENGTH: 734
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                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-10-205-923-10

i Sequence 10, Application US/10205823

i Publication No. US203010896331

i GENERAL INFORMATION:
    APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Gennavarapu, Manjula

APPLICANT: Gennavarapu, Manjula

APPLICANT: Gennavarapu, Manjula

APPLICANT: Gentacheva, Bella

APPLICANT: Gentacheva, Bella

APPLICANT: Morsey, Angela M.

APPLICANT: Angerta, Schubhangi

APPLICANT: Angerta, Karen

APPLICANT: Anderson, Dustin

TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: WUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-08-22

PRIOR FILING DATE: 2001-08-22
                           NVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIE 180
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  QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
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                                                                               MHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKIATTG
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GENERAL INFORMATION:
APPLICANT: Schlagel, Robert
APPLICANT: Badeey, Wilson O.
APPLICANT: Badeey, Wilson O.
APPLICANT: Badeey, Wilson O.
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Angela
APPLICANT: Ganavarapu, Angela
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monesy, Angela M.
APPLICANT: Anderson, Dustin
APPLICANT: MINTON: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: HTHRAPY OF PROSTATE CANCER
TITLE OF INVENTION: NUMBER: 08/10/205, 823
CURRENT FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 66/325,020
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 355
LENGTH: DATE: 2001-03-05
LENGTH: 355
LENGTH: 2007-03-05
LENGTH: 355
LENGTH: 2007-03-05
LENGTH: 355
LENGTH: 2007-03-05
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99.7%; Pred. No. 5.1e-310;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                      SSDEOPESESEPKG 734
                                                                                                                                                                                                                                                                                                              721 SSDEOPESESEPKG 734
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US-10-205-823-8
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Sequence 19, Application US/10473603
Publication No. US20040235066A1
GENERAL INFORMATION:
APPLICANT: OLD, Lloyd
APPLICANT: OLD, Lloyd
APPLICANT: CHEN, Yao-Teng
FILE REFERENCE: LO461.70155USO
CURRENT APPLICATION NUMBER: US/10/473,603
CURRENT APPLICATION NUMBER: DCT/US02/09808
PRIOR FILING DATE: 2003-09-30
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-06-30
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US-10-473-603-19
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Query Match
Best Local Similarity 99.0%;
Matches 718; Conservative
 ORGANISM: Homo sapiens
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   ; ORGAN1SM: нс
US-10-205-823-6
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TISLESLAVILAQLELSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFA
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                                                                                                                                                                                                                                                                                 209 YNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELMIDENKIATTGEANELLHTF
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                                                                                 29 LGKLYTDQDFDSLPAQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNP
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                                                                10 LGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNF
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753;
 Length
                                Indels
Score 3898; DB 14;
Pred. No. 2.9e-304;
1; Mismatches 6;
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US-10-227-884-90
IS-10-227-884-90
| Sequence 90, Application US/10227884
| Publication No. US20030027988A1
| GENERAL INFORMATION:
| APPLICANT: Baker, Kevin P.
| APPLICANT: Generous Luc
| APPLICANT: Gerritsen, Mary
| APPLICANT: Goddard, Audrey
| APPLICANT: Godowski, Paul J.
| APPLICANT: Grimaldi, J. Christopher
| APPLICANT: Gurney, Austin L.
| APPLICANT: Smith, Victoria
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PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
PRIOR PELING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-19
PRIOR PILING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-17
PRIOR PELING DATE: 1998-09-17
PRIOR PELICATION NUMBER: 60/101738
PRIOR PELING DATE: 1998-09-24
PRIOR PELING DATE: 1998-10-28
PRIOR PELING DATE: 1998-10-28
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PRIOR PELING DATE: 1998-11-17
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PRIOR PELING DATE: 1998-11-17
PRIOR PELING DATE: 1998-11-13
PRIOR PELING DATE: 1999-10-12
                                                                                                                                                                                    R APPLICATION NUMBER: 60/099812
R FILING DATE: 1998-09-10
R FILING DATE: 1998-09-10
R FILING DATE: 1998-09-10
R APPLICATION NUMBER: 60/100038
R FILING DATE: 1998-09-11
R FILING DATE: 1998-09-11
R FILING DATE: 1998-09-15
R FILING DATE: 1998-09-15
                                          FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099803
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099811
FILING DATE: 1998-09-10
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FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/126773
FILING DATE: 1999-03-29
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FILING DATE: 1999-02-10
APPLICATION NUMBER: 60/123618
FILING DATE: 1999-03-10
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FILING DATE: 1998-08-31
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Geddawd, Audrey
APPLICANT: Goddawd, Paul J.
APPLICANT: Goddawd, Paul J.
APPLICANT: Goddawd, Paul J.
APPLICANT: Gurneld, J. Christopher
APPLICANT: Gurneld, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L
                                                                                                                                                                        CCDFRICVLKDGAKCYKGLCCKDCQILQSGVECRPKAHPECDIAENCNGSSPECGPDIIL 477
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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Publication No. US20030036635A1
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38.3%; Score 1524.5; DB 14; Length
Best Local Similarity 41.1%; Pred. No. 2.1e-113;
Matches 310; Conservative 134; Mismatches 259; Indels
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R APPLICATION NUMBER: 60/164418
R FILING DATE: 1999-11-09
R APPLICATION NUMBER: 60/166361
R FILING DATE: 1999-11-16
R APPLICATION NUMBER: 60/169445
                                    R FILING DATE: 1999-04-05

R APPLICATION WUMBER: 60/130232

R FILING DATE: 1999-04-26

R FILING DATE: 1999-04-26

R FILING DATE: 1999-04-26

R APPLICATION WUMBER: 60/131270

R APPLICATION WUMBER: 60/131291

R APPLICATION WUMBER: 60/131291

R FILING DATE: 1999-04-27

R APPLICATION WUMBER: 60/13145

R FILING DATE: 1999-06-28

R FILING DATE: 1999-06-14

R APPLICATION WUMBER: 60/14050

R FILING DATE: 1999-06-22

R FILING DATE: 1999-06-22

R FILING DATE: 1999-06-22

R APPLICATION WUMBER: 60/14053

R APPLICATION WUMBER: 60/14052

R APPLICATION WUMBER: 60/14652

R APPLICATION WUMBER: 60/14652

R APPLICATION WUMBER: 60/14659

R FILING DATE: 1999-06-23

R APPLICATION WUMBER: 60/14659

R FILING DATE: 1999-07-26

R APPLICATION WUMBER: 60/14659

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R APPLICATION WUMBER: 60/146963

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| NUMBER: 60/082804<br>1998-04-22<br>NUMBER: 60/08441<br>1998-05-06<br>1998-05-13<br>1998-05-13<br>NUMBER: 60/08532<br>1998-05-15<br>NUMBER: 60/086392<br>1998-05-15<br>NUMBER: 60/08953<br>1998-06-17<br>1998-06-17                                        | 106-18<br>11 (00-24<br>12 (00-24<br>13 (00-24<br>14 (00-24<br>15 (00-24<br>16 (00-24<br>16 (00-24<br>16 (00-24<br>17 (00-24<br>18 (00-24<br>18 (00-24<br>19 | NUMBER: 60/099811<br>1998-09-10<br>1998-09-10<br>NUMBER: 60/099816<br>1998-09-10<br>NUMBER: 60/10038<br>1998-09-11<br>NUMBER: 60/10038<br>1998-09-15<br>NUMBER: 60/100390<br>1998-09-15<br>NUMBER: 60/100390<br>1998-09-15<br>NUMBER: 60/10048<br>1998-09-18<br>NUMBER: 60/10048<br>NUMBER: 60/10138<br>1998-09-18<br>NUMBER: 60/101738<br>1998-09-24<br>NUMBER: 60/101741<br>1998-09-24<br>NUMBER: 60/101741<br>1998-09-24<br>NUMBER: 60/101741                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| PRIOR PILING DATE: 1998-00-28
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Best Local Similarity 41.1%; Pred. No. 2.1e-113;
Matches 310; Conservative 134; Mismatches 259;
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           NR FILING DATE: 1999-08-31

DR APPLICATION NUMBER: 60/164418

DR FILING DATE: 1999-11-09

DR APPLICATION NUMBER: 60/166361

DR APPLICATION NUMBER: 60/16945

OR RILING DATE: 1999-11-16

OR APPLICATION NUMBER: 60/16945

OR APPLICATION NUMBER: 60/169495

OR APPLICATION NUMBER: 60/169895

OR PILING DATE: 1999-12-07
 APPLICATION NUMBER: 60/151733
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; Sequence 90, Application US/10230338 ; Publication No. US20030044934A1

US-10-230-338-90

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Augrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Vetcoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANTION NUMBER: US/10/230,338
CURRENT APPLICATION NUMBER: US/10/19,480
FRIOR PILING DATE: 1997-10/119,480
FRIOR APPLICATION NUMBER: 60/062287
FRIOR APPLICATION NUMBER: 60/063113
FRIOR PILING DATE: 1997-10-28
FRIOR PILING DATE: 1997-10-21
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FRIOR PILING DATE: 1997-10-21
FRIOR PILING DATE: 1998-03-227
FRIOR APPLICATION NUMBER: 60/069973
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  Query Match 38.3%; Score 1524.5; DB 14; Length 787; Best Local Similarity 41.1%; Pred. No. 2.1e-113; Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps
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  , ORGANISM: Homo
US-10-230-338-90
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   APPLICANT: WOOD, WILLIAM 1.

TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P5330P1C14

CURRENT APPLICATION NUMBER: U5/10/218,631

CURRENT FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 60/065913

PRIOR APPLICATION NUMBER: 60/06287

PRIOR APPLICATION NUMBER: 60/063849

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06349

PRIOR PILING DATE: 1997-10-21

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PRIOR PLING DATE: 1997-12-17

PRIOR PLING DATE: 1998-03-26

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PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-27

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  :| | | | | | | : : | | | | | | | : : | - TTAIVLARKQLKKWFAKE---EEFPSSESKSEG 726
  701 LIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG 734
  Desnoyers, Luc
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
   Sequence 90, Application US/10218631 Publication No. US20030045687A1 GENERAL INFORMATION:
   APPLICANT: Baker, Kevin P.
  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
  657
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18;
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   DB 14; Length 787;
  Query Match 38.3%; Score 1524.5; DB 14; Lengt Best Local Similarity 41.1%; Pred. No. 2.1e-113; Matches 310; Conservative 134; Mismatches 259; Indels
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   ; Sequence 90, Application US/10230414; Bublication No. US20030050448A1; GENERAL'INFORMATION:
APPLICANT: Baker, Kevin P.; APPLICANT: Desnoyers, Luc; APPLICANT: Gerritsen, Mary; APPLICANT: Goddard, Audrey; APPLICANT: Goddweki, Paul J.; APPLICANT: Grimaldi, J. Christopher
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-90
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```
PAPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin L.

ALTIE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REPERBRENCE: PS350P10111

CURRENT FILING DATE: 2002-08-29

FRICA FILING DATE: 1002-04-09

FRICA FILING DATE: 1997-10-17

FRICA FILING DATE: 1997-10-17

FRICA FILING DATE: 1997-10-31

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FRICA FILING DATE: 1997-12-17

FRICA FILING DATE: 1997-12-17

FRICA FILING DATE: 1998-03-26

FRICA FILING DATE: 1998-03-27

FRICA FILING 
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   701 LIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG 734
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   Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
  Sequence 90, Application US/10232224
Publication No. US20030065147A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
   ; ORGANISM: Homo Sapien
US-10-232-224-90
  Query Match
Best Local Similarity
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APPLICANT: Gurney, Austin L.
APPLICANT: Sarith, Victoria
APPLICANT: Sarith, Victoria
APPLICANT: Sarith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wacanabe, Colin L.
APPLICANT: Wacanabe, Colin L.
TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-04-09
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FRIOR PELING DATE: 1997-10-17
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FRIOR PELING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/064103
FRIOR PELING DATE: 1997-10-17
FRIOR PELING DATE: 1998-03-26
FRIOR APPLICATION NUMBER: 60/079294
FRIOR PELING DATE: 1998-03-26
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FRIOR FRIOR FILING DATE: 1998-03-26
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ORGANISM: Homo Sapien
  US-10-230-414-90
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PRIOR PILING DATE: 1997-09-17
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APPLICANT: Besnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guriney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Matches
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APPLICANT: Geddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
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  APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victorial
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APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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38.3%; Score 1524.5; DB 14; Length 787;
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APPLICANT: Baker, Kevin P.
APPLICANT: Gerriteen, Mary
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APPLICANT: Grimaldi, 7. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, victoria
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| NUMBER: 60/082804<br>1998-04-22<br>NUMBER: 60/08441<br>1998-05-06<br>1998-05-13<br>NUMBER: 60/085323<br>NUMBER: 60/085323<br>NUMBER: 60/08532<br>1998-05-15<br>NUMBER: 60/089532<br>1998-06-17<br>NUMBER: 60/089532<br>1998-06-17<br>NUMBER: 60/089538<br>1998-06-17<br>NUMBER: 60/089538<br>NUMBER: 60/089538<br>NUMBER: 60/089538 | NUMBER: 60/090472<br>11998-06-24<br>11998-06-24<br>11998-06-25<br>NUMBER: 60/090691<br>11998-06-25<br>NUMBER: 60/091982<br>11998-06-25<br>NUMBER: 60/091982<br>11998-07-07<br>NUMBER: 60/091982<br>11998-08-04<br>11998-08-10<br>NUMBER: 60/095916<br>11998-08-10<br>NUMBER: 60/095916<br>11998-08-10<br>NUMBER: 60/095916<br>11998-08-10<br>NUMBER: 60/095916<br>11998-08-10<br>NUMBER: 60/095916<br>11998-08-10<br>NUMBER: 60/095916<br>11998-09-10<br>NUMBER: 60/095916<br>11998-09-10<br>NUMBER: 60/095916<br>11998-09-09<br>NUMBER: 60/095918<br>11998-09-09<br>NUMBER: 60/095918<br>11998-09-09<br>NUMBER: 60/099598<br>11998-09-09                                                        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PRIOR FILING DATE: 1998-09-24

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  DB 14; Length 787;
  Query Match
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Sequence 90, Application US/10227883; Publication No. US20030073817A1

US-10-227-883-90

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APPLICANT: Stephan, Jenn-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFREENCE: PS320PLC78
CURRENT APPLICATION NUMBER: U0/119, 480
PRIOR APPLICATION NUMBER: 10/119, 480
PRIOR PILING DATE: 2002-04-09
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PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PLING DATE: 1997-10-17
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  R FILING DATE: 1999-03-25

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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Goddard, Audrey
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  APPLICATION NUMBER: 60/112422
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FILING DATE: 1998-09-09
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51; Gaps

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   538 KYVFCGWRNLICGRLVCTYPTRKPFHQENGDVIYAFVRDSVCITVDYKLPRTVPDPLAVK 597
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   418 CCDFRTCVLKDGAKCYKGLCCKDCQILQSGVECRPKAHPECDIAENCNGSSPECGPDITL 477
  471 QTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
   701 LIAIMVKVNFORKKWRTEDYSSDEOPESESEPKG 734
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Human Human

Perfect score:

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Scoring table:

Word size :

**Total** 

Database

Searched:

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Human and mouse sperm protein PH30 beta chain and related DNA - useful in contraceptive vaccines.
  Human PH30 beta chain sperm protein, having a FEE integrin binding domain, is 58.9% identical to mouse and 56.5% identical to guinea pig PH30 beta. The protein may be produced recombinantly and used in a contraceptive composition containing an effective adjuvant and an amount of sperm protein which is effective for the stimulation of antibodies which bind to sperm protein in vivo, thereby preventing or substantially reducing the rate of sperm-egg fusion
   Human PH30 beta chain sperm protein; contraceptive;
FEE integrin binding domain.
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84. .734
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   Human PH30 beta chain sperm protein
  AAR87037 standard; protein; 734 AA
  GF;
  95WO-US007295
   94US-00264101
  Gupta SK, Hollis
(MERI ) MERCK & CO INC
   WPI; 1996-058212/06.
N-PSDB; AAT07328.
Sequence 734 AA;
   Homo sapiens
   WO9535118-A1
  06-JUN-1995;
   20-JUN-1994;
   30-SEP-1996
   28-DEC-1995
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Prostate
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  Human
   Novel
  Novel
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   734
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  January 10,
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Result Š. CANCER RES Chen Y;

2002WO-US009808

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us-10-054-683-19

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Diagnosing cancer comprises contacting a biological sample isolated from a subject with an agent that specifically binds to a nucleic acid molecule, its expression product or fragment or an antibody that binds to the product or fragment.
   Claim 36; Page 124-126; 155pp; English
  2001US-0280718P.
2001US-0285154P.
2001US-0327432P.
2002US-00054683.
  old LJ, Scanlan MJ,
   LUDWIG INST
CORNELL RES
  2003-040608/03
   N-PSDB; ABT15727.
  30-MAR-2001; 2
20-APR-2001; 2
05-OCT-2001; 2
22-JAN-2002; 2
                        29-MAR-2002;
       10-OCT-2002
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   540
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   720
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   240
  300
  360
  ISLESLAVILAQLISLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
  420
   FISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEBCDCGFEQDCALIGETCCDIATCRF 420
  480
   480
   WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
  9
   720
   OKNFLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
   120
  9
  9
   RNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNF
   QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE
  NVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIE
  NVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIE
   MHVIVEKQLYNHMGSDTTVVAQKVPQLIGLTNAIFVSFNITIILSSLELWIDENKIATTG
   WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ
  RNQRCVSSSYLGYDCTTDXCNDRGVCNNXKHCHCSASYLPPDCSVQSDLWPGGSIDSGNF
  EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPRT
  ISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH
  FISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRP
  KAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQ
   CGKLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMVIKDGTSCGSNKVC
   PPVAIPARL PERRYIENI YHSKPMRWPFFLFI PFFIIFCVLIAIMVKVNFQRKKWRTEDY
   MWVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLM
                        Gaps
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The invention comprises a method for diagnosing cancer, the method involves detecting the DNA or protein sequences of human cancer/testis (CT) antigens that are disclosed in the invention. The method of the invention is useful for detecting/diagnosing, treating and monitoring a cancer or condition characterised by the expression of a human CT antigen. The present amino acid sequence represents a human CT antigen
  KAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQ
   WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ
  1 WWVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLM
   QXMFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE
  NVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIE
   MHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELMIDENKIATTG
   EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPRT
  ISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH
   FISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF
   ö
  6; Length 734;
  Indels
  ;
0
   Query Match 100.0%; Score 734; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 734; Conservative 0; Mismatches
  Sequence 734 AA;
  invention
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antigen

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cancer; cancer/testis antigen;

Human; gene therapy; vaccine;

WO200278526-A2 sapiens

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Human cancer/testis

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  The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal cancer, and may be useful in gene therapy. Sequences given in ADB755117-ADB75612 represent marker cDNA and proteins. Note: The sequence of data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
  RNORCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNF 660
  PPVAI PARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDY 720
181 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
   RNORCVSSSYLGYDCTTDXCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNF 660
   CGKLI CKYVGKFLLQI PRATI I YANI SGHLCI AVEFASDHADSQKMWI KDGTSCGSNKVC
  PPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDY
  Ē,
  Gorbatcheva
Anderson D;
  treating
  WO, Gannavarapu M,
I, Glatt K, Zhao X,
  or
   cancer; cytostatic; gene therapy; marker.
  nucleic acid molecule, useful for diagnosing
   Disclosure; SEQ ID NO 10; 99pp; English.
   , Endege WO Wonsey AM,
   ADB75186 standard; protein; 734 AA
   Prostate cancer marker protein.
  25-JUL-2001; 2001US-0307982P.
22-ANG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341146F.
05-MAR-2002; 2002US-0362158P.
  (MILL-) MILLENNIUM PHARM INC
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   SSDEQPESESEPKG 734
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  (first entry)
   I R, Monaire.
S, Kamatkar S, F
  Monahan JE,
   WPI; 2003-248033/24.
  WO2003009814-A2
  Homo sapiens
  04-DEC-2003
   06-FEB-2003
   Schlegel R.
Hoersh S,
   Prostate;
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   900
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  720
   420
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   720
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  9
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  KAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQ
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  PPVAIPARLPERRYIENIYHSKPMRWPFFLFFFIIFCVLIAIMVKVNFQRKKWRTEDY
                                  Gaps
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FEE integrin binding domain.
                                  ö
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  SSDEQPESESEPKG
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  481
  541
  601
   601
  661
  199
   721
  721
  AAR87034;
  361
   AAR87034
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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal control non-prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence date for this patient did not form part of the printed specification, but was obtained in electronic formed directly from WIPO at
                                     625 VCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPM 684
  VLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQK
   New nucleic acid molecule, useful for diagnosing or treating prostate
  Gorbatcheva
Anderson D;
   RWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG 651
   ;
0
   RWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYSSDEQPESESEKG
  Endege WO, Gannavarapu M,
onsey AM, Glatt K, Zhao X,
  Prostate, cancer, cytostatic, gene therapy, marker,
   1,
  DB 7;
  86.0%; Score 631; DB
99.9%; Pred. No. 0;
:ive 0; Mismatches
   Claim 4; SEQ ID NO 8; 99pp; English
   R, Monahan JE, Endege WC
, Kamatkar S, Wonsey AM,
  Ź
  ADB75184 standard; protein; 735
   Prostate cancer marker protein.
  2001US-0307982P.
2001US-0314356P.
2001US-0325020P.
   22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
   25-JUL-2002; 2002WO-US023913
   (MILL-) MILLENNIUM PHARM INC
   (first entry)
  Conservative
   WPI; 2003-248033/24.
   Similarity
   Sequence 735 AA;
  WO2003009814-A2
  Homo sapiens
  25-JUL-2001;
  04-DEC-2003
  Local Simines 731;
  06-FEB-2003
   685
  ADB75184;
   602
  Schlegel
  Query Match
   Hoersh
   cancer,
  Best Loca
Matches
   RESULT 5
ADB75184
ADB75184
ADB75184
ADB75184
ADB75184
ADB75184
ACC The CCC The
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   셤
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   mouse sperm protein PH30 beta chain and related DNA - useful in
  ODFONFCHYQGYIEGYPKSVVMVSTCTGLRGVLOFFNVSYGIEPLESSVGFEHVIYQVKH 144
   204
  AFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDD 241
  122 FQLIGLTNAIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRWKTSYLVLRPHDV 181
  VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMC 361
   NISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRG 624
  NISGHLCIAVEFASDHADSQKWHIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRG 541
  domain, may be recombinantly produced by vector-mediated gene expression in host cells, preferably mammalian cells e.g. Chinese hamster ovary (CHO) cell culture. It may be used in a contraceptive composition containing an effective adjuvant and an amount of sperm protein which is effective for the stimulation of antibodies which bind to sperm protein in vivo, thereby preventing or substantially reducing the rate of spermeng fusion. The protein is also useful for identifying small molecules that disrupt sperm-egg interaction and fertilization
  62 KKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKV 121
   FOLIGLTNAI FVSFNITILISSLELWIDENKIATTGEANELLHTFLRWKTSYLVLRPHDV 264
  AFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDD 324
   325 INKCOCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFISKOKSOCLHNOPRLDPFFKOOA 384
   VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMC 444
  RPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVE 504
   362 RPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVE 421
  FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYA 564
   ODFONFCHYOGYIEGYPKSVVMVSTCTGLRGVLOFENVSYGIEPLESSVGFEHVIYQVKH 61
   KKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKV
  0; Gaps
  Human PH30 beta chain sperm protein, having an FEE integrin binding
  DB 2; Length 651;
   0; Indels
   88.6%; Score 650; DB
100.0%; Pred. No. 0;
ive 0; Mismatches
   Disclosure; Page 29-31; 85pp; English.
   Hollis GF
  95WO-US007295
   94US-00264101
  al Similarity 100.
650; Conservative
   contraceptive vaccines.
   (MERI ) MERCK & CO INC
   Alves K, Gupta SK,
   WPI; 1996-058212/06
  N-PSDB; AAT36700
  Sequence 651 AA;
  06-JUN-1995;
  20-JUN-1994;
                               WO9535118-A1
   28-DEC-1995
   Human and
   385
   N
  422
  82
   145
   205
  265
   182
  242
  302
  445
  505
   Query Match
Best Local
   Matches
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The invention relates to newly discovered cancer markers associated with the cancercus state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the normal level of expression of the marker in the patient sample and the normal cancer.

Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB7561 represent marker cDNA and proteins. Note: The sequence cata for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but
   INKCQCSGAVCIMPEAIHFSGVKIFSNCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQA 403
   VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMC 463
   FQLIGLTNAIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRWKTSYLVLRPHDV 264
   AFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDD 324
   INKCOCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFISKOKSOCLHNOPRLDPFFKOOA 384
  QDFQNFCHYQGYIEGYPKSVVWVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVIXQVKH
   RPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQMICIDGVCMSGDKQCTDTFGKEVE
  FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYA
  NISGHLCIAVEFASDHADSQKMMIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRG
   FQLIGLTNAIFVSFNITILLSSLELMIDENKIATTGEANELLHTFLRWKTSYLVLRPHDV
   VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMC
   RPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVE
   FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYVGKFLLQIPRATIIYA
   QITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNFRVYSYSGTGIMKPLD
  QDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVIYQVKH
  KKADVSLYNEKDI ESRDLSFKLQSAEPQQDFAKY I EMHVI VEKQLYNHMGSDTTVVAQKV
  nucleic acid molecule, useful for diagnosing or treating prostate
   Сарв
  Gorbatcheva
Anderson D;
  ö
   7; Length 753
  1; Indels
  , Gannavarapu M,
Glatt K, Zhao X,
   8
  Score 609; DB; Pred. No. 0; 0; Mismatches
   ğ
  , Endege WO,
Wonsey AM,
  Claim 4; SEQ ID NO 6; 99pp; English
  83.0%;
 05-MAR-2002; 2002US-0362158P.
                               (MILL-) MILLENNIUM PHARM INC.
   Query Match
Best Local Similarity 99.9
Matches 709; Conservative
  R, Monahan JE
Kamatkar S,
  Sequence 753 AA;
  Schlegel R,
Hoersh S,
   25
   44
  82
   104
  145
  205
  224
  265
  284
   325
  344
   385
  404
   445
  464
   505
  565
  524
 #X#X##X#X##X#X##X
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  요
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  셤
  ò
   663
  242
   NELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGRACDANYAGGVVLHPRTIS 303
  362
   422
   482
   542
  543
   602
   KLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKVCRN 603
   662
  722
  VAIDARLPERRYIENIYHSKPMRWPFFLFIPFFIIPCVLIAIMVXVNFORKKWRTEDYSS 723
   363
  483
  QRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPP
NFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENV
                   NFL PHNFR VYSYSGTGI MKPLDQDFQNFCHYQGYI EGYPKSVVMVSTCTGLRGVLQFENV
  NELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGKMCDANYAGGVVLHPRTIS
   LESLAVILAQLLSLSHMITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFI
  SKOKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKA
   GSNCAEGPCCENCLFMSKERMCRPSFEECDLPBYCNGSSASCPENHYVOTGHPCGLNOWI
  CIDGVCMSGBKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG
  LESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAHFI
   GSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWI
   CIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG
   KLICKYVGKFLLQIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKVCRN
  QRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPP
   VAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYSS
  marker
  Prostate; cancer; cytostatic; gene therapy;
  Ŕ
  standard; protein; 753
   cancer marker protein.
   25-JUL-2001; 2001US-0307982P.
22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
   25-JUL-2002; 2002WO-US023913
  (first entry)
   DEOPESESPYG
  DEOPESESEPKG
  WO2003009814-A2.
   Homo sapiens
  04-DEC-2003
                                64
   184
  243
   244
   664
  ADB75182
   Prostate
 63
  183
  303
  304
   363
   364
   423
  424
   483
  484
   543
  544
   603
   604
  663
  723
  724
   ADB75182,
```

283

343

444

504 523 564

144 163 204 583

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Novel proteins comprising contain a disintegrin and metalloprotease domain, referred as ADAM and ADAM polynucleotides for diagnosing, preventing and treating cancer, inflammatory, reproductive,
   ABJ26664 standard; protein; 668 AA.
                                      22-FEB-2001; 2001WO-US005497.
  03-MAR-2000; 2000US-0187937P.
  (HUMA-) HUMAN GENOME SCI INC.
   cardiovascular disorders.
   WPI; 2001-596823/67.
   Ruben SM;
  N-PSDB; AAD18168.
 WO200166557-A1.
                    13-SEP-2001,
  ABJ26664;
  Shi Y,
   RESULT 8
  ABJ26664
ID ABJ;
XX
AC ABJ;
XX
  a
  Human; ADAM protein, a disintegrin and metalloprotease domain, cancer, adamalysin, angiogenic disorder; chronic inflammatory disorder; ARDS; rheumatorid arthritis; adult respiratory distress syndrome; asthma; crohn's disease; atheroscalerosis, macular degeneration; psoriasis; diabetic retinopathy; Alzheimer's disease; tissue remodalling; and abbetic retinopathy; Alzheimer's disease; tissue remodalling; autoimmune disorder; haematopoidetic disorder; infectious disease; HIV-induced dementia; Human immunodeficiency virus; arrhythmia; epilepsy; pulmonary disorder; central nervous system disorder; renal disorder; pulmonary disorder; central nervous system disorder; renal disorder; respiratory disorder; central nervous system disorder;
VCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPM 684
  644 VCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNPPPVAIPARLPERRYIENIYHSKPM 703
  RWPFFLFIPFFIIFCVLIAIMVKVNFORKKWRTEDYSSDEOPESESEPKG 734
  RWPFPLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG 753
   Human gene 2 encoded ADAM protein HOEKN33, SEQ ID NO:7.
   food additive; food preservative; gene therapy
  Location/Qualifiers
   AAE10823 standard; protein; 568 AA
  /note= "Epitope"
340. .358
/note= "Epitope"
   100. .105
/note= "Epitope"
188. .193
   418. .423
/note= "Epitope"
456. .472
/note= "Epitope"
   /note= "Epitope"
268. .274
  84. .291
note= "Epitope"
  note= "Epitope"
  33. .548
note= "Epitope"
  552. .568
/note= "Epitope"
   86. .93
/note= "Epitope"
  note= "Epitope"
  note= "Epitope"
   note= "Epitope"
   "Epitope"
  . .17
'note= "Epitope"
   "Epitope"
   E. .501
/note= "F
  (first entry)
   .410
   .254
   02. .307
  77. .388
   .77
  'note=
   Homo sapiens
  18-DEC-2001
  AAE10823;
                              625
   685
  704
   Region
  Region
  Region
   Region
   Region
  Region
  Region
  Region
   Region
   Region
   Region
   Region
  Region
  Region
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   Region
  AAE10823
  RESULT
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Colled adamalysins) genes, and AABIOR2-AABIOROctease domain, also called adamalysins) genes, and AABIOR2-AABIORS represent the proceins they encode. ADAM proteins and their corresponding genes are useful for they encode. ADAM proteins and their corresponding genes are useful for they encode. ADAM proteins and their antibodies are useful for displaying the analysis of the invention and their antibodies are useful for displaying and treatment of diseases related to anglogenic condition in a mammal. Sequences of the invention and their antibodies are useful for displaying the actions related to anglogenic disorders such as cancer, and carner metastasis, chronic inflammatory disorders such as rheumatoid arthritis, hepatitis, nephritis, crohn's disease, asthma, adult respiratory distress syndrome (ARDS), atherosclerosis, macular degeneration, diabetic retinopathy, Alzheimer's disease, macular convolving the skeletal system, reproductive system, bone related involving the skeletal system, reproductive system, bone related involving the skeletal system, reproductive system, bone related clisorders, autoimmune disorders, haematopoietic disorders, autoimmune disorders, haematopoietic disorders, arrhythmias, high clisorders infections diseases, HIV-induced dementia, arrhythmias, high disorders of proper neurotransmitter release, epilepsy, stroke, neural, bulmonary, proliferation, respiratory (e.g. allergy) disorders and/or cancerous diseases or conditions such as gastric, ungointestinal least home and breast). central nervous system disorders or antagonist prevents skin aging due to sunburn, modulate mammalian characteristics such as body height, weight, hair colour, skin, modulate mammalian metabolism, blortythem and britter and preserve and or concerned encoders and compenses or conditions are useful in the variance obesity, cachexia, wasting disease, andorexia and britter sammalian metabolism, blortythmia and are useful in the variance obesity, cachexia, wasting disease, andorexia or o
  ö
  gene therapy. The present sequence represents a human ADAM protein of
  ö
   2.0%; Score 15; DB 4; Length 568; 100.0%; Pred. No. 1.5e-05; ve 0; Mismatches 0; Indels
  100.0%; Pred ...
Claim 11; Page 274-276; 280pp; English.
   117 LQFENVSYGIEPLES 131
  61
  Conservative
   LOFENVSYGIEPLES
  Query Match
Best Local Similarity
watches 15; Conservat
   Sequence 568 AA;
```

Sequence 668 AA;

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Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant; cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antialoctropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; PMOD; protoin modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gratrointestinal; developmental; vesicle trafficking disorder; protein interaction; duug-target interaction; developmental; vesicle trafficking disorder; infection; gene expression profile; human. Human protein modification + maintenance molecule protein SEQ ID No 18. 06-JUL-2001; 2001US-0303445P. 13-JUL-2001; 2001US-0305405P. 09-AUG-2001; 2001US-031442P. 24-AUG-2001; 2001US-0314821P. 29-AUG-2001; 2001US-0314821P. 03-MAY-2002; 2002US-0378205P. 18-JUN-2002; 2002WO-US019360 (first entry) WO2003000844-A2. Homo sapiens. 03-JAN-2003 

(INCY-) INCYTE GENOMICS INC.

Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM; Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H; CJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J; IX, Gletzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG; Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK; Luo W, Sprague WW, Tang YT, Lu Y, Zebarjadian Y; Forsythe IJ, Thangavelu K, Elliott VS, Gandhi AR, Warren BA, Walia NK,

WPI; 2003-184039/18. N-PSDB; ABT23217 New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and infections.

Claim 73; Page 193-194; 225pp; English.

New secreted human LP polypeptides or polynucleotides, useful for treating mammals suffering from conditions associated with aberrant levels of an LP polypeptide, e.g. cancers, osteoporosis, Paget's disease or Alzheimer's disease.

WPI; 2002-454591/48.

N-PSDB; ABK51494

The inventorial charges by an interaction acid sequence at least sequences of 48-1256 amino acids sequences, 94% identical to a sequence of 100% identical to the 28 amino acid sequences, 94% identical to a sequence of 100 acids, 96% identical to a sequence of 100 acids, or 97% identical to a sequence of 242 amino acids, all given in the specification; or a biologically active or immunogenic fragment of the isolated polymeptide. The polymeptides and polymoleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression of protein modification and maintenance of with the decreased expression of protein modification and maintenance of alternates (PMOD), such as cell proliferative diseases (e.g. cancer, atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS, cancer, altergies), neurological disorders (e.g. stroke, parkinson's disease, allergies), neurological disorders (e.g. stroke, parkinson's disease, compensated), vesicle trafficiking disorders, and infections (e.g. bacterial, viral, parasitic, protozoal). These are also confidential in assessing the effects of exogenous compounds on the expression of the fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the crayer polymericotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or the invantion profiles. This sequence represents a human PMOD protein of the polypeptide. The invanctions, and are the invanctions. The invention relates to an isolated polypeptide comprising: any of 28 of the invention

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  Human; LP102; inflammatory disorder; diabetes; bone disease; cardiovascular disease; male reproductive system disease; osteoporosis; Paget's disease; wyeloma; Alzhelmer's disease; contraceptive; liver cancer; growth factor—mediated disease; anaphylaxis; coagulation; sepsis; skeletal muscle dystrophy; asthma; breast cancer.
                Gaps
                ö
Length 668;
               Indels
        1.7e-05;
2.0%; Score 15; DB 6;
100.0%; Pred. No. 1.7e-0
     100.0%; Prec.
   AAU97037 standard; protein; 759 AA.
   Wang H;
  10-OCT-2001; 2001WO-US027759.
   19-OCT-2000; 2000US-0241813P
                               117 LOFENVSYGIEPLES 131
  121 LOFENVSYGIEPLES 135
   13-AUG-2002 (first entry)
     Local Similarity 100.
   Su EW,
  Human LP protein LP102.
   (ELIL ) LILLY & CO ELI.
  Song HY,
   WO200232939-A2.
   Homo sapiens.
  25-APR-2002.
  AAU97037;
Query Match
   .
2
         Best Loca
Matches
  RESULT 9
   AAU97037
   셤
                               8
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The invention relates to isolated human polypeptides designated LP102, LP187, LP190 and LP241, and the polynucleotides encoding them. The LP C LP187, LP190 and LP241, and the polynucleotides encoding them. The LP C Polypeptide or the LP polypeptide agonist is useful for treating a mammal suffering from a disease, condition or disorder associated with aberrant cast the antibodies are useful for treating preventing or dispensing cancers, inflammatory disorders, bone diseases or cardiovascular diseases. In particular, the LP102 polypeptides, polynucleotides or antibodies are useful for disquasing, preventing or treating male reproductive system diseases, osteoporosis, pager's disease. These are also useful as contraceptive agents. The LP187 polypeptides, polynucleotides or reating contraceptive agents. The LP187 polypeptides, polynucleotides or antibodies are national rate baylo polypeptides, polynucleotides or antibodies are conditions. The LP190 polypeptides, polynucleotides or antibodies are useful for disquases and diseases related to coagulation or sepsis. LP241 polypeptides, and diseases related to coagulation or sepsis. LP241 polypeptides, or disbettes are the LP190 polymetodies are as useful especially for ciasquosing, preventing or treating skeletal muscle dystrophy, breast cancer or disbettes. The LP190 polymetodies are also useful for constructing DNA vectors that may be employed in medicine, or for preparing the proteins. Claim 8; Page 131-134; 148pp; English.

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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polypeptides canced human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, rectal tumour or cancer, colon cancer, breast tumour, proteste tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the release of tumour proliferation of normal human dermal cor stimulating the release of tumour proliferation of normal human dermal cor stimulating the release of tumour mecrosis factor-alpha from human blood, for stimulating the release of tumour proliferation of normal human dermal consists and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU831913 represent human PRO
  Score 15; DB 5; Length 787;
Pred. No. 1.9e-05;
0; Mismatches 0; Indels
  protein sequences of the invention
                          Claim 11; Fig 90; 359pp; English.
   Query Match 2.0%; Scc
Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
   25-JUL-2000; 2000US-0220638P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
   121 <u>||||||||||||||</u>
121 <u>|||</u>
   28-AUG-2002; 2002US-00230163
   117 LQFENVSYGIEPLES 131
   23-JUN-2003 (first entry)
   Human PRO polypeptide #45
   Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
  (GETH ) GENENTECH INC.
   WPI; 2003-342045/32.
N-PSDB; ACA66885.
  Sequence 787 AA;
   US2003036635-A1.
or liver tumor.
  Homo sapiens
  20-FEB-2003
   ABU80783;
   tumor.
  RESULT 11
   ABU80783
g
  ö
  One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors suclas lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
  Gaps
   Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
The present sequence represents the amino acid sequence of LP102
  ö
  Score 15; DB 5; Length 759;
Pred. No. 1.9e-05;
   0; Indels
  Mismatches
   AAU83636 standard; protein; 787 AA.
   Local Similarity 100.0%; Proces 15; Conservative 0;
  Human PRO protein, Seq ID No 90.
  25-JUL-2000; 2000US-0220607P.
25-JUL-2000; 2000US-0220624P.
25-JUL-2000; 2000US-0220638P.
  25-JUL-2000; 2000US-0220666P.
26-JUL-2000; 2000US-0220893P.
28-JUL-2000; 2000WO-US020710.
   2000US-0220664P
  2000US-0222425P.
   2000WO-US030873
  2000WO-US023522
  2000WO-US023328
  2000WO-US032678
  29-JUN-2001; 2001WO-US021066
  2.0%;
  117 LOFENVSYGIEPLES 131
  (first entry)
   Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
   (GETH ) GENENTECH INC
   WPI; 2002-172001/22.
N-PSDB; ABK33580.
                            Seguence 759 AA;
  WO200208288-A2.
  10-NOV-2000; 28-NOV-2000; 2
   20-DEC-2000;
28-FEB-2001;
  01-AUG-2000;
22-AUG-2000;
  23-AUG-2000;
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  31-JAN-2002.
   10-MAY-2001
10-MAY-2001
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   AAU83636
ID AAU8
SXS
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**Gaps** 

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Human, PRO polypeptide, secreted and transmembrane protein; anti-PRO antibody, diagnostic assay, gene expression; tumour, cytostatic.
   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
   One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
  The present invention relates to the isolation of novel human PRO
ABU80783 standard; protein; 787 AA.
   Claim 11; Fig 90; 314pp; English.
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polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUS0739-ABUS0860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
   New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or wounds in a mammal.
  The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122
   Human; secreted and transmembrane protein; PRO; cytostatic; antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; pericyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury;
   MI:
  Gaps
  Gerritsen ME, Goddard A, Godowski ÞJ;
Smith V, Stephan JF, Watanabe CK, Wood
  ö
  Length 787;
  0; Indels
   Novel human secreted and transmembrane protein PRO21340.
   USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
  2.0%; Score 15; DB 6; Le
100.0%; Pred. No. 1.9e-05;
ive 0; Mismatches 0;
  ABO33749 standard; protein; 787 AA.
  Claim 11; Fig 90; 314pp; English.
   12-AUG-2002; 2002US-00218631.
  29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
   01-JUN-2001; 2001WO-US017800.
  131
   (first entry)
  117 LOFENVSYGIEPLES
  Conservative
  Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
  (GETH ) GENENTECH INC.
   Query Match
Best Local Similarity
   2003-512315/48.
  N-PSDB; ACD68637.
  Sequence 787 AA;
  arthritis; wound
  US2003045687-AI.
  Homo sapiens
  06-MAR-2003.
   17-SEP-2003
  ABO33749;
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particularly useful for detecting tumours or biotractors. These are particularly useful for detecting tumours or biotractors. These are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of TMP-apha from human blood, for stimulating proliferation or differentiation of chondrocyte cells, for stimulating proliferation or differentiation of chondrocyte colls, for stimulating proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome cleaning libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective calso be used in gene therapy, particularly for replacing a defective cansumembrane PRO polypeptide
  ö
  Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophiebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
nucleotide sequences. The PRO polypeptides or polynucleotides are useful
   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
  Gaps
   One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial
  ö
  Length 787;
  0; Indels
   Novel human secreted and transmembrane protein PRO21340.
  Score 15; DB 6; Le; Pred. No. 1.9e-05;
  Mismatches
  ABU82092 standard; protein; 787 AA.
  Query Match
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Matches 15, Conservative 0;
  25-JUL-2000; 2000US-0220664P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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   121 LOFENVSYGIEPLES 135
   117 LOFENVSYGIEPLES 131
   (first entry)
   Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
  (GETH ) GENENTECH INC.
   WPI; 2003-393229/37.
  N-PSDB; ACA68541
   Sequence 787 AA;
  US2003088063-A1.
  Homo sapiens.
   25-JUN-2003
   08-MAY-2003
  ABU82092;
   RESULT 13
$$$$$$$$$$$$$$$$$$$$$$$$
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13-MAR-2003
   ABJ72272;
   Query Match
Best Local
   RESULT 15
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  The present invention relates to novel human GENSET coding sequences (ACC51060-ACC51115) and proteins (ABR40453-ABR40508). The GENSET sequences are useful for preparing a composition for treating GENSET-related disorders. They can also be used as markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on Southern gels, as chromosome markers or tags to
   The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovaccular, endothelial or angiogenic disorder in a mammal, e.g. cardiox hypertrophy, trauma, cancer, agerestence in a mammal degeneration, atherosclerosis, hypertension, arterial restence is, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
  Gaps
  New GENSET polynucleotides and polypeptides, useful for preparing a composition for treating GENSET-related disorders and as reagents in assays to quantitatively determined levels of GENSET expression in biological samples.
  ö
infarction), endothelial or angiogenic disorders in a mammal
  Score 15; DB 6; Length 787;
Pred. No. 1.9e-05;
   0; Indela
  2.0%; bcc. No. ...
100.0%; Pred. No. ...
  Claim 2; Page 462-463; 505pp; English.
   Human; GENSET; therapeutic; therapy,
  ABR48487 standard; protein; 787 AA
                        Claim 11; Fig 90; 314pp; English
  Human LAP cell surface protein.
  25-MAY-2001; 2001US-0293574P.
15-UUN-2001; 2001US-0298698P.
29-UUN-2001; 2001US-0302277P.
13-UUL-2001; 2001US-0305456P.
  06-AUG-2001; 2001WO-IB001715.
   117 LOFENVSYGIEPLES 131
   121 LOFENVSYGIEPLES 135
   (first entry)
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Best Local Similarity 100.'
Matches 15; Conservative
  Bejanin S, Tanaka H;
   WPI; 2003-129412/12.
  N-PSDB; ACC51094
  Sequence 787 AA;
  GEST ) GENSET.
  WO200294864-A2
  13-JUN-2003
   Homo sapiens
   28-NOV-2002.
  ABR48487;
   RESULT 14
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   The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TNF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or display the stimulation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO
  manufacture
  Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
  " nucleic acid encoding for a PRO protein, useful for the manufactur a medicament for diagnosing or treating tumors or for measuring or
  PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
  Gaps
  Gaps
identify chromosomes, and as reagents in assays to quantitatively determined levels of GENSET expression in biological samples
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  2.0%; Score 15; DB 6; Length 787;
100.0%; Pred. No. 1.9e-05;
iive 0; Mismatches 0; Indels
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1.9e-05;
   Indels
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  detecting expression of an associated gene
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   Claim 11; Fig 90; 315pp; English.
   01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
  121 LQFENVSYGIEPLES 135
  28-AUG-2002; 2002US-00230414
   117 LQFENVSYGIEPLES 131
  06-NOV-2003 (first entry)
   Conservative
   Best Local Similarity 100. Matches 15; Conservative
  as during gene therapy. T
protein of the invention
   Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
  Human PRO21340 protein.
  (GETH ) GENENTECH INC
  Ouery Match
Best Local Similarity
  WPI; 2003-521818/49.
  N-PSDB: ABT44270
  Sequence 787 AA;
   Sequence 787 AA;
   US2003050448-A1.
   Homo sapiens
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117 LQFENVSYGIEPLES 131

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Search completed: January 10, 2005, 22:34:38 Job time : 162 secs

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Minimum DB E Maximum DB E

Database

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US-10-230-90
   JS-10-219-528-90
  Fequence 19, Application US/10054683
Publication No. US20030044813A1
GENERAL INFORMATION
APPLICANT: Old, Lloyd J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Chen, Yao-Tseng
TILE OF INVENTION: Cancer-Testis Antigens
FILE REFERENCE: L0461/7125 (JRV)
CURRENT APPLICATION NUMBER: US/10/054,683
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 60/280,718
PRIOR APPLICATION NUMBER: US 60/285,154
PRIOR FILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-10-05
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  US-10-054-683-19
  US-10-054-683-19
     SEQ ID NO 19
   Н
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  TYPE: PRT
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  Sequence 10, Appl
Sequence 19, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
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Match
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   361 FISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF
  421 KAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQ
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  14;
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PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 74
TYPE: PRT
CORGANISM: Homo sapiens
US-10-205-823-10

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US-10-473-603-19
  121
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  APPLICANT: Schlegel, Wilson E.
APPLICANT: Schlegel, Wilson O.
APPLICANT: Endegel, Wilson O.
APPLICANT: Endegel, Wilson O.
APPLICANT: Endegel, Wilson O.
APPLICANT: Gorbatcheva, Bella
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Hoersch, Schastian
APPLICANT: Amatkar, Shubhangi
APPLICANT: Angela M.
APPLICANT: Anderson, Dustin
APPLICANT: AND APPLICANT THERRY OF REOSTATE CANCER
APPLICANT: AND APPLICANTION: WUMBER: 105/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
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  FISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
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  MHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKIATTG
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   ; Sequence 10, Application US/10205823; Publication No. US20030108963A1; GENERAL INFORMATION:
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120 120 180 180 240 240

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420 420 480 99 99 720

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GENERAL INVORMATION:

APPLICANT: Schlegel, Robert
APPLICANT: Brdege, Walison O.

APPLICANT: Endege, Walison O.

APPLICANT: Endege, Wanjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Ganatkar, Shubhangi
APPLICANT: Anderson, Dustin
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APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Warehoos FOR IDENTIFICATION, AND
ITILE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: NUMBER: 60/31, 982
FRIGR REFERENCE: MRI-04.02-25
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   63
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  183 VIVEKOLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELMIDENKIATTGEA
  3 VLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQK
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  Query Match

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 731; Conservative 0; Mismatches 1, Indele
  Sequence 8, Application US/10205823
Publication No. US20030108963A1
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   181 MHVIVEKQLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITILSSELHIDENKIATTG 240
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Sequence 19, Application US/10473603
Publication No. US20040235066A1
GENERAL INFORMATION:
APPLICANT: OLD, Lloyd
CURENT SERNETHNO: CANCER-TESTIS ANTIGENS
FILE REFERENCE: L0461.70155US00
CURRENT APPLICATION NUMBER: US/10/473,603
CURRENT FILING DATE: 2003-09-30
PRIOR PILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 59
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100.0%; Score 734; E
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163 204

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Sequence 7, Application US/09945676;
Sequence 7, Application US/09945676;
Fatent No. US2002007465A1
GENERAL INFORMATION:
APPLICANT: SAI et al.
TILE OF INVENTION: ADAM POLYNUCLEOLIGES, POLYPEPTICANT:
FILE REFERENCE: PT051P1
CURRENT PFLING DATE: 2001-09-05;
PRIOR PLING DATE: 2001-09-05;
PRIOR PLING DATE: 2000-03-03;
PRIOR PLING DATE: 2000-03-03;
NUMBER OF SEQ ID NOS: 9
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  | Sequence 6, Application US/10205823 | Sequence 6, Application US/10205823 | Sequence 6, Application No. US203011089531 | CENERAL INFORMATION: | CENERAL INFORMATION: | APPLICANT: Schlegel, Robert | APPLICANT: Grandard, John E. | APPLICANT: Grandard, John E. | APPLICANT: Grandardspu, Manjula | APPLICANT: Glatt, Karen | APPLICANT: Anderson, Dustin | APPLICANT: Manderson, Dustin | APPLICANT: Anderson, Dustin | APPLICANT: Anderson, Dustin | APPLICANT: Anderson, Dustin | APPLICANT: AND | TITLE OF INVENTION WURBER: US/10/205,823 | FRIOR APPLICATION NUMBER: 60/3207.982 | FRIOR PLING DATE: 2001-09-25 | FRIOR PLING DATE: 2001-09-25 | FRIOR PLING DATE: 2001-09-25 | FRIOR APPLICATION NUMBER: 60/341,746 | FRIOR FRIOR APPLICATION NUMBER: 60/341,746 | FRIOR FRIOR FRIOR APPLICATION NUMBER: 6
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Gaps
   Sequence 70, Application US/09924340

Publication No. US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Bejanin, Stephane

APPLICANT: Bejanin, Stephane

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US2.REG

CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT FILING DATE: 2001-08-06

PRIOR PLIING DATE: 2001-07-13

PRIOR PLIING DATE: 2001-07-13

PRIOR PLIING DATE: 2001-07-13

PRIOR PLIING DATE: 2001-06-15

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PRIOR FILING DATE: 2001-06-15

SOFTWARE: DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 70

LENGTH: 787
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US-09-992-095B-70

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publication No. US20030157485A1

GENERAL INFORMATION:
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTYON: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US5.DIV
CURRENT FILING DATE: 2003-02-20

PRIOR PRICATION NUMBER: US/09/992,095B

CURRENT FILING DATE: 2001-08-06

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PRIOR PLING DATE: 2001-08-06

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PRIOR APPLICATION NUMBER: US 60/302,277

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   ; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TILLE DE INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
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; CURRENT APPLICATION NUMBER: US/09/992,600A
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| Publication No. US20040142333A1
| GENERAL INFORMATION:
| APPLICANT: Deshun, Lu
| APPLICANT: Song, Ho Yeong
| APPLICANT: Song, Ho Yeong
| APPLICANT: Su, Eric Wen
| APPLICANT: Wangy, He
| TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
| TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
| FILE REFERENCE: X-13974
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  1998-08-04
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PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
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LENGTH: 787
   Sequence 90, Application US/10227884; Publication No. US20030027988A1; CENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc
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APPLICANT Goddard, Audrey
APPLICANT Goddard, Audrey
APPLICANT Goddard, Audrey
APPLICANT Goddard, Paul J.
APPLICANT Grinaldi, J. Cristopher
APPLICANT Grinaldi, J. Cristopher
APPLICANT Smith, Victoria
APPLICANT Smith, Victoria
APPLICANT Smith, Victoria
APPLICANT Scenario, Jean Philippe F.
APPLICANT Scenario, Jean Philippe F.
APPLICANT Watenabe, Colin L.
APPLICANT Watenabe, Colin L.
APPLICANT Watenabe, Colin L.
APPLICANT Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC79
CURRENT APPLICATION NUMBER: U5/10/227,884
CURRENT APPLICATION NUMBER: 60/06313
PRIOR PILING DATE: 1997-10-17
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APPLICANT: Baker, Kevin P.
APPLICANT: Demoyers, Luc; APPLICANT: Gerritsen, Mary; APPLICANT: Godwski, Paul J.; APPLICANT: Grimaldi, J. Christopher; APPLICANT: Grimaldi, J. Christopher; APPLICANT: Grimaldi, J. Christopher; APPLICANT: Smith, Victoria
                PRIOR APPLICATION NUMBER: 66/125775
PRIOR PILLING DATE: 1999-03-23
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FILING DATE: 1999-03-19
APPLICATION NUMBER: 60/125775
  Stephan, Jean-Philippe
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   APPLICANT:
APPLICANT:
APPLICANT:
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OR APPLICATION NUMBER: 60/100919

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OR APPLICATION NUMBER: 60/101738

OR PILING DATE: 1998-09-24

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OR APPLICATION NUMBER: 60/10196

OR PILING DATE: 1998-09-24

OR APPLICATION NUMBER: 60/10196

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OR APPLICATION NUMBER: 60/10196

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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115733
FILING DATE: 1999-01-12
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APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

ALPLOANT: Naccon Milliams and TRANSFERRANG POLYPEPTIDES AND NUCLEIC
TITLE OF THE STREET STORTS -0.0-2
CURRENT FILING DATE: 2002-0.0-2
PRICE PALLOATION NUMBER: 10/119-480
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OR APPLICATION NUMBER: 60/082604
OR FILLING DATE: 1998-04-22
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OR FILLING DATE: 1998-08-11
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
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APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wacanabe, Colin L.
APPLICANT: Wacanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P35310PLG14
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
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PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
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PRIOR PELICATION NUMBER: 60/063287
PRIOR PELICATION NUMBER: 60/063549
PRIOR PELICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR PELICATION NUMBER: 60/069873
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PRIOR PELICATION NUMBER: 60/079294
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  APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
  ORGANISM: Homo Sapien
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100.0%; Pred. No. 1.5e-05;
tive 0; Mismatches 0; Indels
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R APPLICATION NUMBER: 60/166361

R FILING DATE: 1999-11-16

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RELING DATE: 1999-04-26

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RELING DATE: 1999-04-28

RELING DATE: 1999-06-27

RELING DATE: 1999-06-22

RELING DATE: 1999-07-20

RELING DATE: 1999-07-28

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Matches 15; Conservative
   APPLICANT: Baker, Kevin P.
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APPLICATION NUMBER: US/08/765,243
FLING DATE:
CLASSIFICATION: 536
ATTORNEY/AGBWT INFORMATION:
NAME: APPOLLINA, MARY A
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (908)594-3462
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SEQUENCE CHARACTERISTICS:
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GENERAL INCRWATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUMIL K.
APPRESSEE: AMARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
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100.0%; Pred. No. 0;
iive 0; Mismatches
                        NAME: APPOLLINA, MARY A REGISTRATION NUMBER: 34,087 REFERENCE/DOCKET NUMBER: 192 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: GUPTA, SUNIL K.
; TITLE OF INVENTION; CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; COUNTRY: USA
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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   AUDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
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   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEPAK: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
FILING DATE:
  Sequence 2, Application US/08765243
Patent No. 5935578
   APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTI
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
  LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
  GENERAL INFORMATION:
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  COUNTRY:
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  APPLICANT: ALVES, KENNETH
APPLICANT: ALVES, SUNIL K.
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 B. LINCOLN AVENUE
CITY: RAHWAY
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APPLICATION NUMBER: US/08/264,101
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELECPHONE: (908) 594-3462
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. 5693496
GENERAL INFORMATION:
   TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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  AFLLVYREKSNYVGATFQCKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDD 241
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  VCGNAKLEAGEECDCCTEQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMC 361
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ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
   3: MARY A. APPOLLINA
P.O. BOX 2000, 126 E. LINCOLN AVENUE
  Sequence 2, Application PC/TUS9507295
GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVEN
   CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 1924
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
  TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
  TYPE: amino acid
STRANDEDNESS: siz
  CITY: RAHWAY
STATE: NJ
  FILING DATE
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PCT-US95-07295-2
  302
  625
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                                    265
   182
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  362
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  422
   565
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204
   62 KKADVSLYNEKDIESRDLSFKLQSAEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKV 121
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   APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
FILE REPREBENCE: 91.U86.DIV
CURRENT APPLICANTION HUMBER: US/10/000,489
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT APPLICATION NUMBER: US 09/924,340
PRIOR PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
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PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-15
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   Sequence 70, Application US/10000489; Patent No. 6794363; Patent No. 6794363; AENERAL INFORMATION; APPLICANT: Benjanin, Stephane
protein
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us-10-054-683-19.oli.rai

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   Query Match 2.0%; Score 15; DB 4; Length 787; Best Local Similarity 100.0%; Pred. No. 2.7e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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   Indels
  Sequence 34, Application PC/TUS9305640
GENERAL INFORMATION:
APPLICANT: University of Connecticut
TITLE OF INVENTION: Contraceptive Vaccine
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Encok, Smith & Reynolds, P.C.
STREET: Two Militia Drive
  CUUNTER: USA

ZIP: 02173

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPARE: PATENTIN DATA:
APPLICATION NUMBER: PCT/US93/05640
FILING DATE: 19930610
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/897,883
FILING DATE: June 12, 1992
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REFERENCE/POCKET NUMBER: UCT90-01AA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 861-6540
INFORMATION FOR SEQ ID NO: 34:
SEQUINCE CHARACTERISTICS:
  1.6%; Score 12; DB 5; Le
100.0%; Pred. No. 0.00024;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SEG ID NO 70
LENGTH: 787
  117 LOFENVSYGIEPLES 131
  121 LOFENVSYGIEPLES 135
   LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
   605 CVSSSYLGYDCT 616
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Best Local Similarity 100.
Matches 12; Conservative
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  MOLECULE TYPE: peptide PCT-US93-05640-34
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ORGANISM: Homo sapiens
   TOPOLOGY: linear
   Lexington
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; LOCATION: 1..16
US-10-000-489-70
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   STATE: MA
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Sequence 16, Application PC/TUS9305640
GENERAL INFORMATION:
APPLICANT: University of Connecticut
TITLE OF INVENTION: Contraceptive Vaccine
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: MA
   Length 50;
   Sequence 25, Application PC/TUS9305640
GENERAL INFORMATION:
APPLICANT: University of Connecticut
TITLE OF INVENTION: Contraceptive Vaccine
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Leexington
STATE: MA
  MEDIUM TIPE: F.10py disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05640

FILING DATE: 19930610

CLASSIFICATION:
PRICH APPLICATION DATA:
APPLICATION NUMBER: 07/897,883

FILING DATE: JUBS.
APPLICATION NUMBER: 07/897,883

FILING DATE: Jubs.
APPLICATION NUMBER: 22,592

ATTORNEY/AGENT INFORMATION:
NAME: BLOOK, David E.
REGISTRATION NUMBER: 22,592

REGISTRATION NUMBER: 22,592

REGISTRATION NUMBER: 0CT90-01AA

TELEPHONE: (617) 861-6240

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 mming acids
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05640
FILING DATE: 19930610
   1.6%; Score 12; DB 5; Le 100.0%; Pred. No. 0.00025;
  100.0%; Prea. ...
  ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  450 ECDLPEYCNGSS 461
  Conservative
  26 ECDLPEYCNGSS 37
  ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   linear
  amino acid
   Best Local Similarity
Matches 12; Conserv
  STRANDEDNESS:
  COUNTRY: USA
   PCT-US93-05640-16
  Query Match
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Length 735;
  ; Sequence 12. Application PC/TUS9305640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
INVESPONDENCES: 46
; CORRESPONDENCES: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
; STRET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
   Sequence 6, Application PC/TUS9507295
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
   ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
  DB 5;
  Query Match 1.6%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPALIble
OPERATING SYSTEM: PC-DOS/MS-DOS
   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLIAA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-3462
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compati)
OPERATING SYSTEM: PC-DOS
  121 NVSYGIEPLESS 132
   128 NVSYGIEPLESS 139
  MOLECULE TYPE: protein
  TYPE: amino acid
TOPOLOGY: linear
   USA
   COUNTRY: U
ZIP: 07065
   PCT-US93-05640-12
  8
  ö
  Length 735;
  1.6%; Score 12; DB 5; Length 50; 100.0%; Pred. No. 0.00025; tive 0; Mismatches 0; Indels
   Sequence 6, Application US/08765243
| Patent No. 5935578
| GENERAL INFORMATION:
| APPLICANT: ALVES, KENNETH
| APPLICANT: HOLLIS, GREGORY F.
| TITLE OF INVENTION: CONTRACEPTIVE VACCINE
| NUMBER OF SEQUENCES: B
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MARY A. APPOLLINA
| STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
| CITY: RAHWAY
   ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/765,243
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/897,883
FILING DATE: JUNEAL; 1992
ATTORNEY/AGENT INFORMATION:
NAME: BACOK, David E.
REGISTRATION NUMBER: 2,592
REPERENCE/DOCKET NUMBER: UCT90-01AA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
  ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 1924
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594.3462
   : 735 amino acids
amino acid
   Query Match
Best Local Similarity 100.
Matches 12, Conservative
  450 ECDLPEYCNGSS 461
   TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  26 ECDLPEYCNGSS 37
   ; MOLECULE TYPE: protein US-08-765-243-6
  FILING DATE:
CLASSIFICATION: 536
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   PCT-US93-05640-25
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US-08-765-243-6
   COUNTRY:
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
US-08-993-165-16
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US-09-540-448-16
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   Sequence 16, Application US/08993165A
Facent No. 6123923
GENERAL INFORMATION:
APPLICANT: Unger. Evan C
TITLE OF INVENTION:
FILLE REPRENCE: UNGRIZ24
CURRENT APPLICANT: Wu, Yunqiu
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILLE REPRENCE: UNGRIZ24
CURRENT APPLICATION VUBBER: US/08/993,165A
CURRENT PILING DATE: 1997-12-18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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  Sequence 16, Application US/09540448
Patent No. 6403056
GENERAL INFORMATION:
FAPLICANT:
FILE REFERENCE: UNGRIS92
CURRENT APPLICATION NUMBER: US/09/540,448
CURRENT APPLICATION NUMBER: 08/925,353
FRIOR PILING DATE: 2000-03-31
FRIOR PILING DATE: 1997-09-08
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  1.4%; Score 10; DB 4; Length 68; 100.0%; Pred. No. 0.036; cive 0; Mismatches 0; Indele
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  1 EAGEECDCGT 10
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   Gaps
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100.0%; Pred. No. 0.022;
ive 0; Mismatches 0; Indels
   Sequence 23, Application PC/TUS9305640
GENERAL INFORMATION:
APPLICANT: University of Connecticut
TITLE OF INVENTION: Contraceptive Vaccine
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT PAPLICATION DATA:

APPLICATION NUMBER: PCT/US93/05640

FLING DATE: 19930610

CLASSIFICATION DATA:

APPLICATION NUMBER: 07/897,883

FILING DATE: Jupe2

ATTORNEY AGENT INFORMATION:

NAME: Brook, David E.

REFERENCE/DOCKET NUMBER: UCT90-01AA

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 19930610
  Best Local Similarity 100.0%; Pred. No. 0.0 Matches 10; Conservative 0; Mismatches
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/897,883
FILING DATE: JUNE 12, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 02,592
REFERENCE/DOCKET NUMBER: 02,592
REFERENCE/DOCKET NUMBER: 02,593
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
   40 amino acids
  LENGTH: 40 amino acids
  TYPE: amino acid
STRANDEDNESS: single
  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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   10 LEAGEECDCG 19
   linear
   PCT-US93-05640-12
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PCT-US93-05640-23
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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  January 10,
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Total number of hits satisfying chosen parameters:

Word size :

Minimum DB seg length; 0 Maximum DB seg length; 200000000 PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

fertillin beta cha fertilin beta - cr sperm surface prot batroxostatin - ba platelet aggregati platelet aggregati platelet aggregati hemornagic protei trimucin precursor KMDC 1 protein - c KMD-bearing platel applaggin - easter platelet aggregati metalloproteinase disintegrin-like m probable membrane Description SUMMARIES JC4861 G02937 S23403 S13168 A43020 A43020 A37877 JC4342 S43125 S43125 A539412 A539919 A59410 C43019 E43020 C43019 E40003 A40003 C38539 JC7850 S71948 AE0486 S18968 G43019 D43019 8 Query Match Length Result Š

| meltrin gamma - mo | hypothetical prote | probable transport | hypothetical prote | hypothetical prote | metalloproteinase | d-aminoacylase (as | metalloproteinase | jararhagin C precu | catrocollastatin p | ADAM 5 protein pre | fertilin alpha-II | fertilin alpha-I - | hypothetical prote | hypothetical 7K pr | short neurotoxin 1 |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| S60259             | A69227             | A72786             | B64696             | A64573             | A59414            | B75202             | S48169            | S24789             | S55270             | 148100             | 855060            | \$55059            | C71684             | JS0583             | NINJIB             |
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| 151                | 151                | 233                | 394                | 417                | 419               | 526                | 549               | 571                | 609                | 777                | 825               | 905                | 59                 | 9                  | 61                 |
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| 30                 | 31                 | 32                 | 33                 | 34                 | 35                | 36                 | 37                | 38                 | 39                 | 40                 | 41                | 42                 | 43                 | 44                 | 45                 |

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| # 1      | a chain - human  mo sapiens (man)  191996 #sequence_revision 18-Oct-1996 #text_change 09  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  1974861  197 | Hatatus predicted |
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|          | Query Match<br>Best Local Similarity 100.0%; Pred. No. 0;<br>Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 0,                |
| υ Δ      | Qy 1 MWVLFLLSGLGGLRMDSNFDSLPVQ1TVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 60                |
| 0 0      | Oy 61 OKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 120<br>120        |
| O D      | Qy 121 NVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLOSAEPQODFAKYIE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 180<br>180        |
| 0 0      | QY 181 MHVIVEKOLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKIATTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 240               |
| O A      | Qy 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFOGKMCDANYAGGVVLHPRT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 300               |
| O A      | Qy 301 ISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 360<br>360        |
| <i>o</i> | Qy 361 FISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 420               |

us-10-054-683-19.011.rpr

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Matches 10; Conserv
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  fertilin beta - crab-eating macaque
C:Speciee: Macaca fascicularis (crab-eating macaque)
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C;Accession: G02937; S55061
R;Ramarao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
Submitted to the EMBL Data Library, August 1995
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R;Perry, A.C.F.; G1chuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
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C;Accession: S23403; S25696
C;Accession: S23403; S25696
C;Accession: S23402; T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
Nature 356, 248-252, 1992
A;Title: A potential fusion peptide and an integrin ligand domain in a protein active in A;Reference number: S23402; MUID:92204234; PMID:1552944
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KAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQ 480
  WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
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   PPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDY 720
   661 PPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWRTEDY 720
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  117 LQFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQS 168
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   481
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C;Accession: S13168
R;Rucinski, B.; Niewiarowski, S.; Holt, J.C.; Soszka, T.; Knudsen, K.A.
Biochim. Biophys. Acta 1054, 257-262, 1990
A;Title: Batroxostatin, an Arg-Gly-Asp-containing peptide from Bothrops atrox, is a poter A;Reference number: S13168; MUID:91002685; PMID:2207176
  Riscarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, P. C. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities of disintegrins isolated from Ame A;Reference number: A43019; WUID:93123215; PMID:8419314
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  platelet aggregation disintegrin (jararacin), venom - jararacussu
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C;Accession: A43020
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
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ive 0; Mismatches 0; Indels
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C;Accession: 847570; 843125
R;Taai, I.H.; Wang, Y.M.; Lee, Y.H.
B;Cohim. Biophye. Acra 1200, 337-340, 1994
A;Title: Characterization of a cDNA encoding the precursor of platelet aggregation inhib A;Reference number: 847570; MUID:94347824; PMID:8068721
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R;Barker, H.L.; Perry, A.C.F.; Jonnes, R.; Hall, L.
Bicchim. Biophye. Acta 1218, 429-431, 1994
A;Title: Sequence and expression of a monkey testicular transcript encoding tMDC I, a no A;Reference number: 847645; MUID:94325353; PMID:8049267
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C;Date: 27-Jan_1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
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hemorrhagic protein HR1B - habu
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c;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37877
R;Takeya, H: 0da, K.; Miyata, T.; Omori-Satoh, T.; Iwanaga, S.
J. Biol. Chem. 265, 16068-16073, 1990
A;Title: The complete amino acid sequence of the high molecular mass hemorrhagic protein
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A;Accession: A37877
A;Status: preliminary
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A43019
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S;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities of disintegrins isolated from Amagnetic number: A43019; MUID:93123215; PMID:8419314
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F;Huang, K.F.; Hung, C.C.; Pan, F.M.; F.M.; Tsugita, A.; Chiou, S.H.
Biochem: Biophys. Res. Commun. 216, 223-233, 1995
A;Title: Characterization of multiple metalloproteinases with fibrinogenolytic activity
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  A; Accession: JC4342
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   analysis.
   Matches
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  A; Accession: A59410
  A; Accession: B43020
  Query Match
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                                  A Molecule type: mRNA
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F;392-477/Domain: disintegrin homology cDIS-
  J. Biochem. 125, 31-35, 1999
Affille: Ussuriatin 2, A Novel KGD-Bearing Disintegrin from Agkistrodon ussuriensis Ve
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A;Accession: A59412
  applaggin - eastern cottonmouth
C;Species: Agkietrodon piscivorus piscivorus (eastern cottonmouth)
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S;Accession: A33990
R;Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chow, E.P.; Marzec, U.M.; Harker, L.A.; Mara
Proc. Nall. Acad. Sci. U.S.A. 86, 8050-8054, 1989
A;Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a potent inhi
A;Reference number: A33990; MUID:90046735; PMID:2510158
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  Length 71;
  Length 71;
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C;Accession: F43019
R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Chem. 268, 1058-1065, 1993
A;Title: Chem. 268, 1058-1065, 1993
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A;Title: Characterization of the integrin specificities of disintegrins isolated from Ame A;Reference number: A43019; MUID:93123215; PMID:8419314
  Fukuoka Univ. Sci. Reports 30, 71-78, 2000
A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloydiu
A;Reference number: A59409
  platelet aggregation disintegrin (brevicaudin) 1b, vemon - Gloydius halys brevicaudus
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  Length 73;
  Length 72;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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"Molecular cloning of the human fertilin beta subunit.";
Biochem. Biophys. Res. Commun. 224:118-326(1996).
  Hall L., Frayne J.; "Nucleotide sequence of the human fertilin beta transcript."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Tourestion and interfaces."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)

-1- FUNCTION: Sperm surface membrane protein that may be involved in sperm-e9g plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with e9g membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the e9g. This is a non catalytic metalloprotease-like protein.

-1- SUBCELLULAR LOCATION: Type I membrane protein.
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G0:0005178; F:integrin binding; TAS.
G0:0008237; F:metallopeptidase activity; TAS.
G0:0007342; P:fusion of sperm to egg plasma membrane; TAS.
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Alternative splicing; Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
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N-linked (GloNAC.)
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   REDURES 2238825; Pubbled = 12477932; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Strausberg R.L., Seberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunarane P.H., Alton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton B.K., Ketreman M., Madan A., Young A.C., Shevychenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Stalska M.J., Schmutz J., Myers R.W., Butterfield Y.S., Answill M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
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Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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CARBOHYD
CARBOHYD
  DISULFID
   DISULFID
  CARBOHYD
  CARBOHYD
   DISULFID
   DISULFID
  DISULFID
  SIGNAL
  PROPEP
  DOMAIN
  HERTISLESLAVILAQLISLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFE 231
  TCRFKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPC 476
  297 HPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFE 356
  DFAHFISKOKSOCLHNOPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIA 416
  TCRFKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPC 351
  GLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEA 536
  GLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEA 411
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
   MEDLINE=96341733; PubMed=8720115; Ramarao C.S., Myles D.G., White J.M., Primakoff P.; Ramarao C.S., Myles D.G., White J.M., Primakoff P.; Initial evaluation of fertilin as an immunocontraceptive antigen and molecular cloning of the cynomolgus monkey fertilin beta subunit."; Mol. Reprod. Dev. 43:70-75(1996).
  Gaps
  MEDLINE=95260313; PubMed=7741716;
Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
"Cloning and analysis of monkey fertilin reveals novel alpha subunit
  Q28478, Q28412;
Q28478, Q28472;
Q28-FEB-2003 (Rel. 41, Created)
Q58-FEB-2003 (Rel. 41, Last sequence update)
G5-JUJ-2004 (Rel. 44, Last annotation update)
G5-JUJ-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
AMM=ADAM2; Synonyms-FTNB;
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cercopithecinae; Macaca.
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
MCBI_TaxID=9541;
   ö
  Length 579;
   0; Indels
  SEQUENCE FROM N.A.
TISSUB-Brain;
Strausberg R.;
Submitted (DEC. 2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC064547; AAH64547.1; -.
   547; AAH64547.1; -.
579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;
   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
  32.8%; Score 241; DB 2; Le
100.0%; Pred. No. 1.7e-233;
ive 0; Mismatches 0;
  735 AA
  Biochem. J. 307:843-850(1995).
  Matches 241; Conservative
   STANDARD;
   Similarity
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  D 537
  Ď 412
   TISSUE=Testis;
  357
   352
  172
  232
   417
   292
  477
  537
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   SEQUENCE
  Query Match
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218 SFNITIILSSLELWIDENKI 237
  NCBI_TaxID=9986;
  MEROPS; M12.950;
  AD02 RABIT
Q28660;
   RESULT 6
AD02_RABIT
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  ö
  Luiversity, Cambridge, United Kingdom.

EMBL: AJ309003; CAG4225.2; -.

REMBL: AJ309003; CAG4225.2; -.

REMBL: AJ309003; CAG4225.2; -.

REMBL: AJ309003; CAG64225.2; -.

REMBL: AJ309003; CAG64225.2; -.

REMBL: AJ309003; CAG64225.2; -.

REGO: GO:00003676; F:nucleic acid binding; IEA.

RGO: GO:0003676; F:nucleic acid binding; IEA.

RGO: GO:0003676; F:nucleic acid binding; IEA.

R GO: GO:0003676; F:nucleic acid binding; IEA.

R InterPro: IPR00589; P:proteolysis and peptidolysis; IEA.

R InterPro: IPR00589; Publicegrin.

R InterPro: IPR00199; Nucleic acid OB.

R InterPro: IPR00199; Peptidase_MI2B.

R InterPro: IPR001990; Peptidase_MI2B.

R Pfam; PF002200; Disintegrin; 1.

R Pfam; PF002209; PG1180290; PG1180299; 1.

R Pfam; PF00421; Repropep; 1.
  Gaps
   Gaps
  118 LQFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQS 169
   117 LOFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLQS 168
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
   TISSUE=Testis;
MEDLINE=22872989; PubMed=14510675;
Day A.E., Quilter C.R., Sargent C.A., Mileham A.J.;
Chromosomal mapping, sequence and transcription analysis of the porcine fertilin beta gene (ADAM2).";
Anim. Genet. 34:375-378(2003).
 N-linked (GlcNAc. .) (Potential).
S -> T (in Ref. 2).
BE84BE115E1D0B53 CRC64;
  ö
   2.7%; Score 20; DB 2; Length 735; 100.0%; Pred. No. 1.4e-10; ive 0; Mismatches 0; Indels
   7.1%; Score 52; DB 1; Length 735; 100.0%; Pred. No. 7.4e-43; ive 0; Mismatches 0; Indels
  3F 3; 1.
81804 MW; 16F5554690AEF4AE CRC64;
  Created)
Last sequence update)
Last annotation update)
   PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS50026; EGF 3; 1.
SEQUENCE 735 AA; 81804 MW; 16F5;
  PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
SMART; SM00608; ACR; 1.
SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
 566 566 N-
723 723 S
735 AA; 82357 MW;
   Q866A8;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
   52; Conservative
  Best Local Similarity 100.
Matches 20; Conservative
  PRELIMINARY;
   Query Match
Best Local Similarity
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   Sus scrofa (Pig).
  NCBI_TaxID=9823;
   Fertilin beta.
  TISSUE=Testis;
  Name=FTNB;
CARBOHYD
CONFLICT
SEQUENCE
  Query Match
  Q866A8
   Matches
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   -:- SUBUNIT: Hererodimer with ADAMI/fertilin alpha.
-:- SUBUNIT: Hererodimer with ADAMI/fertilin alpha.
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SUBCELLULAR LOCATION: Expressed specifically in testis.
-:- DOMAIN: A trippeptide motif (VGE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (My similarity).
-:- FTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
-:- SIMILARITY: Contains I disintegrin domain.
-:- SIMILARITY: Contains I EGF-like domain.
  MEDLINE=97071141; PubMed=8914066;

MEDLINE=97071141; PubMed=8914066;

Hardy C.M., Holland M.K.;

Holland M.K.;

Holland M.K.;

Holland M.K.;

Mol. Reprod. Dev. 45:107-116(1996).

-I FUNCTION: Sperm surface membrane protein that may be involved in apperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between ite disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
58-FEB-2003 (Rel. 41, Last sequence update)
65-UTL-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
(Fertilin beta subunit) (PH-30) (PH30) (PH30-beta)
Name-ADAM2; Synonyms-FTNB;
Oryctolagus cuniculus (Rabbit)
  751 AA
   InterPro; IPR005586; ADAM cysteine.
InterPro; IPR00742; EGF 2.
InterPro; IPR00742; EGF 2.
InterPro; IPR006742; EGF 2.
InterPro; IPR006209; EGF 11ke.
InterPro; IPR008994; NucTeic_acid OB.
InterPro; IPR008994; NucTeic_acid OB.
InterPro; IPR0028970; Peptidase_M12B.
InterPro; IPR00280; Disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolyalin; 1.
PRIVES; PR004289; DISINTEGRIN; 1.
SWART; SW006684; Disintegrin; 1.
SWART; SW006089; DISINTEGRIN; 1.
PROSITE; PS00427; DISINTEGRIN; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS00129; EGF 1; FALSE NEG.
   EMBL; U46070; AAA93321.1; -.
HSSP; P30403; 1N4Y.
STANDARD;
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217 SFNITIILSSLELWIDENKI 236

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633
735 AA;
  Query Match
Best Local Similarity
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DISULFID
  DISULFID
DISULFID
SEQUENCE
  DISULPID
  DOMAIN
TRANSMEM
   DISULFID
  PROPEP
CHAIN
   DOMAIN
  SIGNAL
  DOMAIN
ö
   "The precursor region of a protein active in sperm-egg fusion contains a metalloprotease and a disintegrin domain: structural, functional, and evolutionary implications.";
Proc. Natl. Acad. Sci. U.S.A. 90:10783-10787(1993).
   "A potential fusion peptide and an integrin ligand domain in a protein active in sperm-egg fusion."; Nature 356:248-252(1992).
-I- FUNCTION: Sperm surface membrane protein that may be involved in
  Gaps
       n; Glycoprotein; Signal; Transmembrane.
Potential.
   TISSUE=Testis;
MEDINE=94068486; PubMed=8248170;
Wolfsberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,
   TISSUE=Testis;
MEDLINE=92204234; PubMed=1552944;
Blobel C.P., Wolfsberg T.G., Turck C.W., Myles D.G., Primakoff P.,
   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 44, Last annotation update)
ADAM 2 precursor (Alaintegrin and metalloproteinase domain 2)
(Fertilin beta subunit) (FH-30) (FH30).
Name-ADAM2; Synonyms=FTNB;
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
   (Potential)
   (Potential)
   (Potential)
  (Potential)
  ö
   Potential
Potential
  (Potential)
  2.7%; Score 20; DB 1; Length 751;
100.0%; Pred. No. 1.4e-10;
tive 0; Mismatches 0; Indels
   824C6FBFC4A9FCE1 CRC64;
   Extracellular (Potential)
   Cytoplasmic (Potential).
Metalloprotease-like.
Disintegrin-like.
  (GlcNAc.
  (GlcNAc.
  (GlcnAc
   (GlcNAc
   (GlcNAc
  (GlcNAc
   (GlcnAc
   735 AA.
   Potential.
By similarity.
By similarity.
   EGF-like.
By similarity.
                        By similarity.
   By similarity.
   By similarity
N-linked (Glo
   Potential.
   Linked
   N-linked
  N-linked
  N-linked
  Linked
   PRT;
                                  ADAM 2
  217 SFNITILISSLELWIDENKI 236
  217 SFNITIILSSLELWIDENKI 236
PROSITE, PS50026; EGF 3; 1.
Cell adhesion; EGF-like domain;
  83616 MW;
  SEQUENCE OF 383-735 FROM N.A.
   Local Similarity 100.
hes 20; Conservative
   STANDARD;
   751 AA;
   SEQUENCE FROM N.A.
  NCBI_TaxID=10141;
   AD02 CAVPO
Q60411;
                                 CHAIN
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DOMAIN
DOMAIN
   DOMAIN
DOMAIN
DISULFID
  CARBOHYD
CARBOHYD
CARBOHYD
  CARBOHYD
SEQUENCE
  DISULFID
   Query Match
   CARBOHYD
  DISULFID
   DISULFID
  CARBOHYD
  CARBOHYD
  CARBOHYD
  CARBOHYD
   DISULFID
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   PROSITE; PS50215; AJAM MEPRO; 1.
PROSITE; PS50215; DISINITEGRIN 1; 1.
PROSITE; PS50214; DISINITEGRIN 2; 1.
PROSITE; PS50022; EGF 1; FALSE NEG.
PROSITE; PS50026; EGF 2; FALSE_NEG.
PROSITE; PS50026; EGF 3; 1.
Cell adhesion; EGF-1ike domain; Glycoprotein; Signal; Transmembrane.
  DB 1; Length 735;
1.4e-08;
   By similarity.
By similarity.
By similarity.
7535FC39F44FB645 CRC64;
  Extracellular (Potential)
Potential.
  Cytoplasmic (Potential).
Metalloprotease-like.
Disintegrin-like.
   By similarity.
By similarity.
Potential.
  By similarity.
ADAM 2.
  MEROPS; M12.956; -.
InterPro; IPR001565; ADAM cysteine.
InterPro; IPR001762; Disintegrin.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR006210; IEGF.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR001590; Peptidase M12B.
Ffam; PF00200; Disintegrin; 1.
Pfam; PF01421; ReproJysin; 1.
PRINTS; PR00289; DISINTEGRIN; 1.
PRODOM; PF000064; Disintegrin; 1.
  Score 18;
Pred. No.
   Cys-rich.
EGF-like.
  81904 MW;
  2.5%; 8
  EMBL; Z11720; CAA77784.1; -. HSSP; P18619; 1FVL.
  SMART; SM00608; ACR; 1.
SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
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TISSUESTEFACTOR N.A.

TISSUESTEFACTOR N.A.

SEQUENCE FROM N.A.

SUZUKI O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,

Matsumuco K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,

Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,

Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,

Kuga N., Kuroda A., Satoh I., Kamata K., Takahashi E., Kataohima Y.,

Matanabe M., Sugiyama T., Irle R., Otsuki T., Sato H., Wakamatsu A.,

Ishii S., Yamashita H., Matsuo K., Nakamura Y., Satio K., Nishikawa T.,

Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,

Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,

Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

BMBL; AK122608; BAC85489:1; --

RINTETPO: IPRO012870; Peptidase M12B.

RINTETPO: IPRO012870; Peptidase M12B.

RINTETPO: IPRO1281; Reptidase M12B.

RR Pfam; PPO1421; Reptilyshin; 1.
PS01186; EGF_2; FALSE_NEG.
PS50026; EGF_3; 1.
domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
   Length 746;
  0; Indels
  Cyconiasmic (Potential).
Metalloprotease-like.
Disintegrin-like.
Cys-like.
  1D8C7E9071502E30 CRC64;
   Extracellular (Potential)
  Last sequence update)
Last annotation update)
   DB 1; Le
1.5e-06;
   (Glenac.
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   (GlcNAc.
  (GlcNAc
   (GlcNAc
   [G] CNAC
   (Glcnac
  By similarity.
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By similarity.
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   2.2%; Sco...
100.0%; Pred. No....
0; Mismatches
  PRT; 279 AA.
  Potential.
ADAM 18.
  Potential
   Potential
   Created)
  PROSITE; PS50215; ADAM MEPRO; 1
  05-UUL-2004 (TYENBLREI. 27, Cre 05-UUL-2004 (TYENBLREI. 27, Las 05-UUL-2004 (TYENBLREI. 27, Las Hypothetical protein FLJ16017. Homo sapiens (Human)
  84448 MW;
  117 LOFENVSYGIEPLESS 132
   118 LQFENVSYGIEPLESS 133
   Conservative
  PRELIMINARY;
   294
359
   Local Similarity
hes 16; Conserv
  746 AA;
   NCBI_TaxID=9606;
                                       PROSITE; 1
EGF-like
  DOMAIN
TRANSMEM
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   DISULFID
  CARBOHYD
CARBOHYD
   DISULFID
  DISULPID
  DISULFID
   CARBOHYD
   CARBOHYD
  CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
  CARBOHYD
  SEQUENCE
   Query Match
   PROPEP
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  SIGNAL
  Q6ZWL1
  Matches
  RESULT 9
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          ö
   prepubertal testis.

DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).

FTM: The prodomain and the metalloprotease-like domain are cleaved during the epididymal maturation of the spermatozoa.

SIMILARITY: Belongs to peptidase family M12B.

SIMILARITY: Contains I disintegrin domain.
  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
20.1-0CT-2004 (Rel. 45, Last annotation update)
ADAM IS precursor (A disintegrin and metalloproteinase domain 18)
(Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-rich protein III) (tMDC III)
Name-ADAM18; Synonyme-FIVDC3;
  Prayne J., Jury J.A., Barker H.L., Perry A.C.F., Jones R., Hall L.;
Prayne J., Jury J.A., Barker H.L., Perry A.C.F., Jones R., Hall L.;
"Macaque MDC family of proteins: sequence analysis, tissue
distribution and processing in the male reproductive tract.";
Mol. Hum. Reprod. 4:429-437(1998).
-!- FUNCTION: Sperm surface membrane protein that may be involved in
spermacogenesis and fertilization. This is a non catalytic
metalloprotease-like protein (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed predominantly in adult and
       Gaps
  Macaca fassicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
          ö
          Indels
          ö
   Prodom; PD000664; Disintegrin; 1.
SMART; SM00608; ACR; 1.
SMART; SM00505; DISIN; 1.
PROSITE; PSS0215; ADAM_MEPRO; 1.
PROSITE; PSS0214; DISINTEGRIN 1; FALSE_NEG.
PROSITE; PSS0214; DISINTEGRIN 2; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
       0; Mismatches
  InterPro; IPR006586; ADAM cysteine. InterPro; IPR001762; Disintegrin. InterPro; IPR001762; EGF 2.
InterPro; IPR005299; EGF 1ike.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
  255 SYLVLRPHDVAFLLVYRE 272
  EMBL; Y08617; CAA69909.1; -. HSSP; P83469; 1MPZ.
   18; Conservative
  Cercopithecinae; Macaca.
  STANDARD;
  SEQUENCE FROM N.A.
   MEROPS; M12.957;
   TISSUE=Testis;
  AD18 MACFA
Q95194;
  AD18 MACRA
AD18 MACRA
AD18 MACRA
AD 8 MACRA
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 01-0CT-
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787 AA;
   SEQUENCE FROM N.A.
TISSUE=Testis;
   SEQUENCE FROM N.A.
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  rissum=Testis;
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  Strausberg R.
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   Asiababia N., Aotsuka S., Shoji T., Ichihara T., Shichata N., Asiabaki N., Aotsuka S., Shoji T., Ichihara T., Shichata N., Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y., A matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa S., Kariyama S., Catoh N., Matsumawa H., Takahashi E., Kataoka R., Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y., Matanabe M., Sudyyama T., Irite R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamashita H., Matsuo Y., Nakamira Y., Sato K., Nishikawa T., Kiwchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Kiwchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugano S., Nagahari K., Masukuo Y., Nagai K., Isogai T.; Subanitted (Juli-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (Juli-2003) to the EMBL/GenBank/DDBJ databases.
   Gaps
  TISSUE=TESTIS,
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feringold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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NCBI_TaxID=9606;
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDMA FL16017 fis, clone TESTI2002618, weakly similar to ADAM 2.
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
A disintegrin and metalloprotease domain 32 (Similar to MDC family).
   Query Match 2.0%; Score 15; DB 2; Length 279; Best Local Similarity 100.0%; Pred. No. 6.6e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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   121 LQFENVSYGIEPLES 135
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  117 LQFENVSYGIEPLES 131
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Matches 15; Conserv
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  121
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RR FER FERU
RR MEDLI
RA KIAUR
RA ALISER
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   NCBI_TaxID=9913;
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   SEQUENCE
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  RESULT 14
AD02_BOVIN
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   RESULT 13
   AAQ89099
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   TISSUE-Testis,

MEDLINE=2238825; PubMed=12477932;

MEDLINE=2238825; PubMed=12477932;

MEDLINE=2238825; PubMed=12477932;

MALGADIA S. F., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S. F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S. F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiywik S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse cDNA sequences."

T and mouse CDNA sequences."

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   Gaps
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  A Strausberg K.,

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

R SEMBL, BC026085; AAH26085.1; -.

R HSSP; P30403; IN4Y.

R HSO; GO: 0004222; F: metalloendopeptidase activity; IEA.

R GO; GO: 0007229; P: integrin-mediated signaling pathway; IEA.

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R GO; GO: 00007229; P: proceolysis and peptidolysis; IEA.

R GO; GO: 00006209; P: proceolysis and peptidolysis; IEA.

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DR InterPro; IPR00280; Peptidase_M12B.

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DR Pfam; PF0121; ReprojVsin; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JMR-2004 (TrEMBLrel. 26, Last annotation update)
A disintegrin and metalloprotease domain 32.
Name=bAM32;
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
  787 AA
  PRT;
  Probon, PD000664; Disintegrin; 1. SMART; SM00608; ACR; 1. SMART; SM00509; DISIN; 1. SWART; SM0181; EGF; 1. PROSITE; PS50215; ADAM_MEPRO; 1.
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  SEQUENCE FROM N.A.
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  TISSUE=Testis;
   Q8TC42
   RESULT 12
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10 GTC42
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  "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: Bioinformatica Assessment.";
Bioinformatica Assessment.";
Bioinformatica Assessment.";
BMBL; AX358739; AAQ69099.1;
  PubMed=12975309;
Clark H.F. Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd is
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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Mammalla; Eutheria; Cetartlodactyla; Ruminantia; Pecora; Bovidae;
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   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
(Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
BOB taurus (Bovine)
   ;
0
  2.0%; Score 15; DB 2; Length 787;
100.0%; Pred. No. 1.6e-05;
ive 0; Mismatches 0; Indels
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PROSITE; PS01186; BGF 2; UNKNOWN 1.
PROSITE; PS50026; BGF 3; 1.
Integrin; Metalloprotease; Protease.
SEQUENCE 787 AA; 87931 MW; CE0F54AS0466B336 CRC64;
  7/39; AAQ89099.1; -. 787 AA; 87933 MW; 3D84CACFECCIA12E CRC64;
  Last sequence update)
Last annotation update)
  2.0%; Score 15; DB 2; Le
100.0%; Pred. No. 1.6e-05;
iive 0; Mismatches 0;
   787 AA
   745 AA
   Created)
   PRT:
  117 LOFENVSYGIEPLES 131
  121 LOFENVSYGIEPLES 135
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  117 LOFENVSYGIEPLES 131
   121 LOFENVSYGIEPLES 135
   Ouery Match
Best Local Similarity 100.v
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Les 15; Conservative
   PRELIMINARY;
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   Similar to MDC family. UNQ5982.
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DISULFID
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CARBOHYD
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  SEQUENCE
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   homolog
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  RESULT 15
   Q8BJ80
   S444444448
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
   SUBUNIT: Heterodimer with ADAMI/fertilin alpha.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed specifically in testis.
TISSUE SPECIFICITY: Expressed specifically in testis.

TISSUE Atripaptide motif (TDE) within dishitegrin-like domain bowain: A tripaptide motif (TDE) within dishitegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).

FTM: The signal and the metalloprotesse domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
SIMILARITY: Belongs to peptidase family MI2B.
SIMILARITY: Contains I dishitegrin domain.
SIMILARITY: Contains 1 EGF-like domain.
   complex.";
Biol. Reprod. 56:1245-1254(1997).

Biol. Reprod. 56:1245-1254(1997).

Function: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
                           Waters S.I., White J.M.; "Biochemical and molecular characterization of bovine fertilin alpha and beta (ADAM 1 and ADAM 2): a candidate sperm-egg binding/fusion
   \overline{\text{EGF-like}} domain; Glycoprotein; Signal; Transmembrane.
  Extracellular (Potential)
   Cytoplasmic (Potential)
   Metalloprotease-like
  Disintegrin-like
   Potential.
By similarity.
  similarity.
  InterPro; IPR006586; ADAM_cysteine.
InterPro; IPR001762; Disintegrin.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 1.
InterPro; IPR006210; IEGF.
InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR001590; Peptidase Mi2B.
InterPro; IPR001590; Peptidase Mi2B.
   Cys-rich.
EGF-like.
Poly-Ser.
By similar
   Potential
  PRINTS; PRO1289; DISINTEGRIN.
PRODOM; PRO10664; DiSINTEGRIN; 1.
SMART; SM00069; ACK; 1.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS0186; EGF 1; FALSE_NEG.
PROSITE; PS0186; EGF 2; FALSE_NEG.
PROSITE; PS0186; EGF 2; FALSE_NEG.
PROSITE; PS01026; EGF 1; FALSE_NEG.
  ADAM 2.
   propep; 1
              MEDLINE=97304362; PubMed=9160725
   Pfam, PF00200; Disintegrin, 1.
Pfam, PF01562; Pep M12B propep
Pfam, PF01421; Reprolysin; 1.
   EMBL; AF086808; AAC62753.1; -.
  P18619; 1FVL.
   MEROPS; M12.950;
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  SIGNAL
   ROPEP
   DOMAIN
  DOMAIN
  CHAIN
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   STRAIN=CS7BL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
   STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
   Gaps
   STRAIN=CS7BL/6J; TISSUB=Testis;
MEDIINE=20530913; PubMed=11076861;
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Schibata K., Itch M., Alzawa K., Kitsunai T., Tashiro H., Itch M.,
   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:1700008E04 product:METALLOPROTEASE/DISINTEGRIN
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   ..
  (Potential)
  DB 1; Length 745;
0.00015;
nes 0; Indels
  B5D8DC0168999B00 CRC64;
By similarity.
Potential.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc..
   STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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100.0%; Pred. No. ...
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N-linked
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MEDLINE-21085660; Pubmed-11217851;
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   118 LQFENVSYGIEPLE 131
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S-09-026-001A-6
S-09-460-295B-13
  Sequence 8, Application US/08765243

Patent No. 5935578

GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GRECORY F.
ITLE OP INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 536
ATTORNEY/AGETT INCORMATION:
NAME: APPOLLINA, MARY A
REGIGTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 8:
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REGISTRATION NUMBER: 34,087
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TELEPHONE: (908) 594-3462
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SOFTWARE: Patentin Release #1.0, Version #1.30
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FILING DATE:
CLASSIFICATION:
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APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHMAY
CONTRACTORN AVENUE
CITY: RAHMAY
CONTRACTORN AVENUE
CITY: RAHMAY
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240
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Length 734;
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624

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   89.1%; Score 3551; DB 2; Length 651; 100.0%; Pred. No. 4.3e-284; ive 0; Mismatches 0; Indels
   CAPTION TYPE: Floppy disk

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
FLING DATE:
CLASSIFICATION: 536
ATTONNEY/AGENT INPOMMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 34,087
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (908)594-3462
   APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: GUPTA, SUNIL K.
APPLICANT: GUPTA, SUNIL K.
TILLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
  Sequence 2, Application US/08765243
Patent No. 5935578
  TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
   651 amino acids
  Best Local Similarity 100.0
Matches 650; Conservative
  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
  MOLECULE TYPE: protein
  GENERAL INFORMATION:
   USA
   07065
   COUNTRY:
  RESULT 4
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  US-08-765-243-2
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   요
  KKADVSLYNEKDIESRDLSFKLQSAEPQQPFAKYIEMHVIVEKQLYNHMGSDTTVVAQKV 121
   FQLIGLTNAIFVSFNITIILSSLELMIDENKIATTGEANELLHTFLRWKTSYLVLRPHDV 181
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   89.1%; Score 3551; DB 1; Length 651; 100.0%; Pred. No. 4.3e-284;
   0; Indels
   STATE: No.

COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:

COMPUTER PLODRY disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,101
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAWE: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (908) 594-3462
TELEPHONE: (908) 594-3462
TELEPAX: (908) 594-4720
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

"TELEPAX: 651 amino acids
                         GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: ALVES, KENNETH
APPLICANT: HOLLIS, GENEGORY F.
ITILE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
  100.0%; Prec. ...
                Sequence 2, Application US/08264101
Patent No. 5693496
  LENGTH: 651 amino acids TYPE: amino acid
   Matches 650; Conservative
  single
  MOLECULE TYPE: protein
  Best Local Similarity
   TOPOLOGY: linear
  STRANDEDNESS:
   US-08-264-101-2
   385
  8
  62
  205
  122
   182
  325
   Query Match
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MOLECULE TYPE: protein

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  542 VCNNKKHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPM 601
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   Sequence 2, Application PC/TUS9507295

SEQUENCE 2, Application PC/TUS9507295

SEQUENCE 3, SEQUENCE 3, SEQUENCE 3, SEQUENCE 4, SEQUENCE 5, TITLE OF INVENTION: CONTRACEPTIVE VACCINE NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: MAX A. APPOLLINA STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE 5, CITY: RAHMAY
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/07295
  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELECHNOWE: (908)594-3462
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acids
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
   USA
  STATE: NJ
COUNTRY: US
ZIP: 07065
   FILING DATE:
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   Indela
   89.1%; Score 3551; DB 5; Lv
100.0%; Pred. No. 4.3e-284;
tive 0; Mismatches 0;
   ALURESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
   APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
ITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   Sequence 6, Application US/08765243; Patent No. 5935578; GENERAL INFORMATION:
  Matches 650; Conservative
   Query Match
Best Local Similarity
   USA
  07065
;
PCT-US95-07295-2
  COUNTRY:
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  3 VLFLLSG---LGGL---RMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYT
  Indele
  Sequence 6, Application PC/TUS9507295
; Sequence 6, Application PC/TUS9507295
; GENERAL INFORMATION:
APPLICANT: GUFTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TILLE OF INVENTON: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
   SOFTWARE: PatentIn Release #1.0, Version #1.30
   Query Match
61.2%; Score 2440; DB 5;
Best Local Similarity 59.6%; Pred. No. 1.9e-192;
Matches 439; Conservative 119; Mismatches 167;
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
   ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELEPHONE: (908) 594-4762
TELEPHONE: (908) 594-4762
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
  LENGTH: 735 amino acids TYPE: amino acid
   MOLECULE TYPE: protein PCT-US95-07295-6
   COMPUTER READABLE FORM:
   CLASSIFICATION:
   USA
   COUNTRY: US
ZIP: 07065
  TOPOLOGY:
   124
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  57 VNLMOKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV 116
  LOFENVSYGIEPLESSVGFEHVIYQVKHKKADVSLYNEKDIESRDLSFKLOSAEPQQDFA 176
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  KYIEMHVIVEKOLYNHMGSDTTVVAQKVFQLIGLTNAIFVSFNITIILSSLELWIDENKI
  SGNFPPVAI PARLPERRYIENIYHSKPMRWPFFLFIPFFIIFCVLIAIMVKVNFQRKKWR
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   12;
   Length 735;
   Query Match 61.2%; Score 2440; DB 2; Length 7 Best Local Similarity 59.6%; Pred. No. 1.9e-192; Matches 439; Conservative 119; Mismatches 167; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
FILING DATE:
CLASSIFICATION: 536
  CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELEPHONE: (908) 594-4462
TELEPHONE: (908) 594-4720
  717 TEDYSSDEQPESESEPK 733
   TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
  LENGTH: 735 amino acide
TYPE: amino acid
  ; MOLECULE TYPE: protein US-08-765-243-6
   TOPOLOGY: linear
   357
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240 LNSKSDISGSCGISAGGYKECPPNDRMCGKIICKYQSENILKLRSATVIYANISGHVCVS 299
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  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
   STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE CITY: RAHWAY
   Sequence 4, Application US/08765243
; Patent No. 5935578
; GENERL INFORMATION:
APPLICANT: AUVES, KENNETH
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVANTION: CONTRACEPTIVE VACCINE
TITLE OF INVANCES: 8
CORRESPONDENCE ADDRESS:
  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELEFAX: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  USA
   FILING DATE:
  07065
  COUNTRY:
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   477 GLNQWICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEA 536
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   38.0%; Score 1512; DB 1; Length 457; 57.6%; Pred. No. 3.1e-116; tive 74; Mismatches 115; Indels
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,101
FILING DATE:
CLASCIPATE:
  ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
  Sequence 4, Application US/08264101
Patent No. 5693496
GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: GUPTA, SUNIL K.
APPLICANT: GUPTA, CONTRACEPTIVE VACCINE
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
OURRESPONDENCE ADDRESS:
  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
  717 TEDYSSDEQPESESEPK 733
  : 457 amino acids
amino acid
  (908) 594-4720
  Conservative
  TELEFAX: (908)594-472
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
  ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  single
   MOLECULE TYPE: protein
   linear
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Best Local Similarity
Matches 265; Conserv
  STRANDEDNESS:
  USA
  STATE: NJ
  COUNTRY:
   LENGTH:
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   GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
ITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 B. LINCOLN AVENUE
CITY: RAHWAY
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
  ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGIGTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INPORMATION:
TELEPHONE: (908)594-3462
   TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
  STATE: NJ
COUNTRY: US
ZIP: 07065
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US-08-765-243-4
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   Gapa
  GRERAL INFUGGANT: Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV.

CURRENT FILING DATE: 2001-11-14

CURRENT FILING DATE: 2001-11-14

PRIOR PLING DATE: 2001-08-06

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

SOFTWARE: JDatent

SEQ ID NO 70

LENGTH: 787

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   Sequence 70, Application US/10000489
Patent No. 6794363
GENERAL INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
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TYPE: amino acid
STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
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Sequence 116, Application US/10140002
Patent NO. 6725730
GENELLINFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers Luc
APPLICANT: Perorgets Luc
APPLICANT: Pivaroff, Ellen

US-10-140-002-116

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  517
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  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC59
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Prior Application removed - See Palm or File Wrapper
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  Stewart, Timothy A. Tumas, Daniel
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  Watanabe, Colin K
Wood, William
  Sherwood, Steven
Smith, Victoria
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   APPLICANT: Cerretti, Douglaa P.
TITLE OF INVENTION: SVPH1-8 DNA and Polypeptides
FILE REFRENCE: 03260.0050-0030/617,145
CURRENT APPLICATION NUMBER: U5/09/617,145
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
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; Sequence 2, Application US/09617145;
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; GENERAL INFORMATION:
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  APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
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   Gao, Wei-Qiang
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  Watanabe, Colin K
   Godowski, Paul J. Gurney, Austin L.
  Sherwood, Steven
  Desnoyers, Luc
Filvaroff, Ellen
  Smith, Victoria
  Goddard, Audrey
   Tumas, Daniel
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   APPLICANT: YOSHIMURA, KOji
APPLICANT: NOSHIMURA, Koji
APPLICANT: HIKICHI, Yuichii
APPLICANT: NISHIMURA, Atsushi
TITLE OF INVENTION: No. 668018961 Protein and DNA Thereof
FILE REFERENCE: 2544 USOP
CURRENT APPLICATION NUMBER: US/09/786,256C
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/JP99/04766
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
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   Query Match
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339 HEMGHNFGMFHDDYS-CKCPSTICVMD-KALSFYIPTDFSSCSRLSYDKFFEDKLSNCLF 396
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  492 DKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICK---- 547
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